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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:37:03 ; Search time 46 Seconds
(without alignments)

1642.475.Million cell updates/sec

Title: US-10-084-018-3

Perfect score: 2554

Sequence: 1 MVGAMKIVSLVLLMPGFC.....RAFDMINRFYKGMWPYVG 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_13Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550	99.8	476	19 AAW72966	Human serine carbo
2	2539	99.4	476	20 AAY28570	Secreted peptide c
3	2539	99.4	476	22 AAU39043	Human secreted pro
4	2539	99.4	476	23 ABB55752	Human polypeptide
5	2538	99.4	476	20 AAY13372	Amino acid sequenc
6	2538	99.4	476	21 AAB01407	Human TANGO 176
7	2538	99.4	476	22 AAU29228	Human PRO polypept
8	2538	99.4	476	22 AAB80240	Human PRO223 prote
9	2538	99.4	476	24 ABU69650	Novel human secret

10	2538	99.4	476	24 ABU71316	Human PRO223 prote
11	2538	99.4	476	24 ABU71473	Human PRO polypept
12	2538	99.4	476	24 ABU71919	Human secreted/tra
13	2538	99.4	476	24 ABU65773	Human secreted/tra
14	2538	99.4	476	24 ABU66106	Novel human secret
15	2538	99.4	476	24 ABU67373	Human secreted pro
16	2538	99.4	476	24 ABU67610	Human secreted/tra
17	2538	99.4	476	24 ABU64527	Human secreted/tra
18	2538	99.4	476	24 ABU65468	Human PRO polypept
19	2538	99.4	476	24 ABU58604	Human PRO polypept
20	2538	99.4	476	24 ABU56140	Human secreted/tra
21	2538	99.4	476	24 ABU57135	Human secreted/tra
22	2538	99.4	476	24 ABU54375	Human secreted/tra
23	2538	99.4	476	24 ABU10714	Human protein sequ
24	2538	99.4	477	22 AAM25810	Human membrane or
25	2536	99.3	476	22 AAB88381	Human hydrophobic
26	2533	99.2	476	22 AAB88587	Human serine carbo
27	2512.5	98.4	477	19 AAW72965	Human serine carbo
28	1772.5	69.4	351	19 AAW72967	Novel human diagno
29	1371	53.7	299	22 ABG22322	Drosophila melanog
30	960.5	37.6	482	22 ABB60774	Human lung tumour
31	557	21.8	480	22 AAB76860	Clone #18991 of lu
32	557	21.8	480	23 AAU85515	Human lung cancer
33	557	21.8	480	24 ABU59487	Lung cancer therap
34	557	21.8	480	24 ABU66389	Human precursor pr
35	553.5	21.8	452	18 AAW15091	Lung cancer associ
36	553.5	21.7	492	21 AAB58436	Human protective p
37	545.5	21.4	438	18 AAW15092	Mouse TANGO 176.
38	538.5	21.1	492	21 AAB01416	Novel human diagno
39	525.5	20.6	102	22 ABG22321	Sequence of protease
40	498.5	19.5	491	15 AAR48059	A. niger carboxype
41	491.5	19.2	612	23 ABR38834	Arabidopsis thalia
42	484	19.0	482	21 AAG30065	Arabidopsis thalia
43	484	19.0	502	21 AAG30064	A. niger carboxype
44	482.5	18.9	536	23 ABR38819	C. albicans BAX-as
45	472.5	18.5	550	23 ABG33281	

ALIGNMENTS

RESULT 1
AAW72966
ID AAW72966 standard; Protein; 476 AA.
XX
XX AAW72966;
XX AC
XX AC
DT 21-JAN-1999 (first entry)
XX
DE Human serine carboxypeptidase MMLR3DF01.
XX
XX Human; serine carboxypeptidase; CPEPT; diabetes mellitus; stroke;
KW Alzheimer's disease; multiple sclerosis; inflammatory glomerulonephritis;
KW atherosclerosis; ischaemic heart disease; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 118 /label= unknown
FT /note= "encoded by TTW"
FT Misc-difference 146 /label= unknown
FT /note= "encoded by STC"
FT
FT
XX WO9844128-A1.
XX
XX
XX PD 08-OCT-1998.
XX
XX
XX 30-MAR-1998; 98WO-US06250.
XX
XX 31-MAR-1997; 97US-0828488.

```
XX (INCY-) INCYTE PHARM INC.
XX Bandnan O, Goli SK, Hawkins PR, Hillman JL, Lal P;
XX WPI; 1998-557121/47.
XX N-PSDB; AAV64076.
XX Novel human serine carboxypeptidase - useful in the treatment of
XX e.g. diabetes mellitus, Alzheimer's disease, multiple sclerosis
XX Claim 1; Page 46-47; 68pp; English.
XX The present sequence represents a human serine carboxypeptidase (CPEPT).
XX The protein can be used in methods to treat disorders associated with
XX increased CPEPT expression e.g. diabetes mellitus, inflammatory
XX glomerulonephritis, atherosclerosis or ischaemic heart disease, or
XX disorders associated with decreased CPEPT expression such as stroke,
XX Alzheimer's, Parkinson's or Huntington's disease, multiple sclerosis or
XX amyotrophic lateral sclerosis. A hybridisation probe, complementary to
XX part of the nucleic acid sequence encoding CPEPT, can be used to detect
XX nucleic acids encoding CPEPT in a sample. Host cells and vectors,
XX containing nucleic acids encoding CPEPT, can be used to express CPEPT.
XX Sequence 476 AA;
XX
XX Query Match 99.8%; Score 2550; DB 19; Length 476;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-241;
XX Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MVGAMWKVIVSLVLLMPCDGLFHSLYRSVSMPPKGDGQPLFLTPYEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPCDGLFHSLYRSVSMPPKGDGQPLFLTPYEAGKIQKREL 60
QY 61 SLVGGPPGLNWKSYAGFLTVNKTYSNLFVWFFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
Db 61 SLVGGPPGLNWKSYAGFLTVNKTYSNLFVWFFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
QY 121 FVEHGPVVTNNMLDRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNMLDRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIQFOIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSLNPRVREKINLNGAIGDGY 240
Db 181 SALIQFOIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSLNPRVREKINLNGAIGDGY 240
QY 241 DPESIIGGYAEFLYQIGLLDEKQKYFQKQCHIEHIRKQNWFEAFIELDKLLDGLTS 300
Db 241 DPESIIGGYAEFLYQIGLLDEKQKYFQKQCHIEHIRKQNWFEAFIELDKLLDGLTS 300
QY 301 DPSYFQNVTCNSYNNFLRCTEBEDQLYYKFLSLPEVROAIHVGNQTFNDGTIVVEKYL 360
Db 301 DPSYFQNVTCNSYNNFLRCTEBEDQLYYKFLSLPEVROAIHVGNQTFNDGTIVVEKYL 360
QY 361 EDTVQSVKPLTEIMNNKYLVINGOLDIIVAALTEKSLMGMDWKGSOBYKAEKKVWK 420
Db 361 EDTVQSVKPLTEIMNNKYLVINGOLDIIVAALTEKSLMGMDWKGSOBYKAEKKVWK 420
QY 421 IFKSDSEVAGYIRQVGDHGVIIIRGGGHILPYDQPLRAFDMINRFYIGKWDPIYG 476
Db 421 IFKSDSEVAGYIRQVGDHGVIIIRGGGHILPYDQPLRAFDMINRFYIGKWDPIYG 476
XX
XX RESULT 2
XX ID AAY28570
XX AC AAY28570;
XX DT 26-OCT-1999 (first entry)
XX DE, Secreted peptide clone bv280_3.
XX
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```
KW Secreted; proliferation; differentiation; cytokine activity; vaccine;
KW anti-inflammatory; tissue growth; tumour inhibition; gene therapy;
KW haematopoiesis regulator; cell proliferation; immune stimulant.
OS Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 10..22
XX Protein /label= signal_peptide
XX /label= bv280_3
XX Active-site 195..212
XX /note= "Serine carboxypeptidase active site motif"
XX
XX WO9336512-A1.
XX 22-JUL-1999.
XX 11-JAN-1999; 99WO-US00550.
XX 08-JAN-1999; 99US-0227462.
XX 13-JAN-1999; 98US-0071304.
XX (GEMY ) GENETICS INST INC.
XX
XX Agostino MJ, Clark HF, Collins-Racie LA, Evans C;
XX Fechtel K, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
XX Spaulding V, Steininger RJ, Treacy M, Wong GG;
XX WPI; 1999-493881/41.
XX N-PSDB; AAZ10805.
XX New polynucleotides encoding human secreted proteins used for
XX therapeutic, diagnostic and research purposes
XX Claim 16; Page 111-113; pp128; English.
XX
XX This sequence is the human secreted protein bv280_3. This protein shows
XX homology to a carboxypeptidase, and has a serine carboxypeptidase active
XX site motif at residues 195-212. Polynucleotides AAZ10804-210813 and
XX polypeptides AAY28568-28590 are predicted to have biological activities
XX which would make them suitable for treating, preventing or ameliorating
XX medical conditions in humans and animals, although no supporting data is
XX given. Suggested activities include nutritional activity, cytokine and
XX cell proliferation or differentiation activity, immune stimulating
XX as vaccines) or suppressing activity, haematopoiesis regulating
XX activity, tissue growth activity, anti-inflammatory activity,
XX cadherin/tumour invasion suppressor activity, and tumour inhibition
XX activity. The polynucleotides may also be useful for gene therapy.
XX
XX Sequence 476 AA;
XX
XX Query Match 99.4%; Score 2539; DB 20; Length 476;
XX Best Local Similarity 99.2%; Pred. No. 2.2e-240;
XX Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 MVGAMWKVIVSLVLLMPCDGLFHSLYRSVSMPPKGDGQPLFLTPYEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPCDGLFHSLYRSVSMPPKGDGQPLFLTPYEAGKIQKREL 60
QY 61 SLVGGPPGLNWKSYAGFLTVNKTYSNLFVWFFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
Db 61 SLVGGPPGLNWKSYAGFLTVNKTYSNLFVWFFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
QY 121 FVEHGPVVTNNMLDRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNMLDRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIQFOIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSLNPRVREKINLNGAIGDGY 240
Db 181 SALIQFOIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSLNPRVREKINLNGAIGDGY 240
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 Db 361 EDTVQSVKPKWLTETIMNNYKVLINYGQDIIIVAAALTEKSLMGMDWKGQSEYKKAKKVWK 420
 QY 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476
 Db 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476

RESULT 3

AAU39043
 ID AAU39043 standard; Protein; 476 AA.

XX AC AAU39043;
 XX DT 16-JAN-2002 (first entry)
 XX DE Human secreted protein bv280_3.
 XX KW Human; secreted protein; antiinflammatory; immunosuppressive;
 KW nootropic; neuroprotective; antiarthritic; antimicrobial; vulnary;
 KW cytostatic; antidiabetic; virucide; antifertility; anticonvulsant;
 KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
 KW antineumatic; antitumor; antitumor; osteopathic; tranquiliser;
 KW cerebroprotective; cytokine; cell proliferation; cell differentiation;
 KW immune deficiency; severe combined immunodeficiency; SCID; tumour;
 KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
 KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
 KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
 KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
 KW food supplement; vaccine.

OS Homo sapiens.

XX W0200175068-A2.

XX 11-OCT-2001.

XX 22-MAR-2001; 2001WO-US09369.

XX 30-MAR-2000; 2000US-0539330.

XX 04-DEC-2000; 2000US-0729674.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie E, Collins-racie LA, Evans C;
 PI Treacy M, Agostino MJ, Steiner RJ, Spaulding V, Wong GG;
 PI Clark H, Fechtel K, Merberg D;

XX WPI; 2001-639363/73.

XX N-PSDB; AAS59261.

XX Secreted human proteins, useful as vaccine for treating various
 PT diseases such as autoimmune disorders (e.g. multiple sclerosis), and
 PT nervous system disorders (e.g. stroke) -

XX Disclosure; Page 529-530; 619pp; English.

XX The invention relates to novel human secreted proteins, the nucleic
 CC acids encoding them. The protein may exhibit cytokine, cell proliferation
 CC or cell differentiation activity or may induce production of other
 CC cytokines in certain cell populations and may exhibit immune stimulating
 CC or immune suppressing activity, which is useful for the treatment of
 CC various immune deficiencies and disorders e.g. severe combined
 CC immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis,

CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary
 CC inflammation. The proteins are also useful in the treatment of diseases
 CC and disorders including tissue, skin and organ transplantation and in
 CC graft-versus-host diseases (GVHD), in the induction of tumour immunity,
 CC myeloid or lymphoid cell deficiencies, wound healing and tissue repair,
 CC in the treatment of burns, incisions and ulcers; as well as in treatment
 CC of periodontal disease, osteoporosis or osteoarthritis, mediated by
 CC inflammatory processes, diseases of the peripheral nervous system,
 CC Alzheimer's, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, and Shy-Drager syndrome, infections,
 CC infarction of cardiac and central nervous system vessel e.g. stroke,
 CC sepsis, inflammatory bowel disease, ulcers, bone regeneration. The
 CC protein, having activin- or inhibin-related activities is useful as a
 CC contraceptive based on the ability of inhibins to decrease fertility in
 CC female mammals and decrease spermatogenesis in male mammals. The
 CC proteins and nucleic acids are also useful as food supplements. The
 CC present sequence represents a secreted protein of the invention.

XX Sequence 476 AA;

Query Match 99.4%; Score 2539; DB 22; Length 476;
 Best Local Similarity 99.2%; Pred. No. 2.2e-240;
 Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMWKIVISLVLLMPGCDGLFHSLYRSVSMPPKGSQGLFLTPYIEAGKIQKREL 60
 Db 1 MVGAMWKIVISLVLLMPGCDGLFHSLYRSVSMPPKGSQGLFLTPYIEAGKIQKREL 60

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 Db 121 FVEHGPVYVTSNMLDRDFPMTTXXSMLYIDNPVGTGFSFTDDTHGYAVNDDVDVARDLY 180

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 Db 301 DPYSFQNVTCGSNNYFNFLRCTEPEDQLYYVKFSLPEVROAIHVGNQTFNDGTIVVEKYL 360

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 Db 361 EDTVQSVKPKWLTETIMNNYKVLINYGQDIIIVAAALTEKSLMGMDWKGQSEYKKAKKVWK 420

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 Db 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476

RESULT 4

ABB55752

ID ABB55752 standard; Protein; 476 AA.

XX ABB55752;

XX 14-FEB-2002 (first entry)

XX Human polypeptide SEQ ID NO 110.

XX Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;
 CC immune disorder; bacterial infection; fungal infection; cancer; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin;
 KW osteoporosis; osteoarthritis; nervous system disorder; neuropathy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; activin;
 KW haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnary;

KW ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic;
 KW Crohn's disease; cytostatic; anti-inflammatory; immunomodulator;
 KW neuroprotective; haemostatic; thrombolytic; anti-inflammatory.

OS Homo sapiens.

XX US2001039335-A1.

XX 08-NOV-2001.

XX 04-DEC-2000; 2000US-0729674.

XX 10-APR-1997; 97US-126425P.

XX 04-DEC-1997; 97US-067454P.

XX 20-DEC-1997; 97US-068379P.

XX 02-JAN-1998; 98US-070346P.

XX 07-JAN-1998; 98US-070643P.

XX 08-JAN-1998; 98US-070755P.

XX 13-JAN-1998; 98US-071304P.

XX 22-JAN-1998; 98US-072134P.

XX 30-JAN-1998; 98US-073095P.

XX 18-FEB-1998; 98US-075038P.

XX 30-MAR-2000; 2000US-0539330.

XX 23-NOV-1998; 98US-0197886.

XX (JACO/) JACOBS K.

XX (MCCO/) MCCOY J M.

XX (LAVA/) LAVALLIE E R.

XX (COLL/) COLLINS-RACIE L A.

XX (EVAN/) EVANS C.

XX (MERB/) MERBERG D.

XX (TREA/) TREACY M.

XX (AGOS/) AGOSTINO M J.

XX (STEI/) STEININGER R J.

XX (SPAU/) SPAULDING V.

XX (WONG/) WONG G G.

XX (CLAR/) CLARK H.

XX (FECH/) FECHTEL K.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;

PI Wong GG, Clark H, Fechtel K;

XX WPI; 2002-040725/05.

XX N-PSDB; ABA90930.

XX New secreted proteins and encoding polynucleotides, useful in gene
 PT therapies, particularly for preventing or treating autoimmune
 PT disorders, cancer, graft-versus-host disease, wound, osteoporosis,
 PT stroke or inflammations

PS Disclosure; Page 255-256; 349pp; English.

XX The invention relates to isolated polynucleotides (ABA90876-ABA90968 and
 CC ABA90980) and encoded proteins (ABBS5698-ABBS5800), especially
 CC polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90985) and
 CC proteins SEQ ID NO 2 (ABBS5698) and SEQ ID NO 20 (ABBS5707) contained in
 CC clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1
 CC are deposited with the American Type Culture Collection (ATCC) with
 CC accession number 98599. The polynucleotides and encoded polypeptides have
 CC cytostatic, anti-inflammatory, immunomodulator, vulnerary,
 CC neuroprotective, activin, inhibin, chemotactic, haemostatic, thrombolytic
 CC and anti-inflammatory activity and acting as cytokine modulators,
 CC haematopoietic regulators, tissue growth modulators and/or cadherin
 CC suppressors. The polypeptides and polynucleotides are useful in gene
 CC therapies, particularly for preventing, treating or ameliorating any of
 CC the following diseases: immune deficiency and disorders; e.g. bacterial
 CC or fungal infections, autoimmune disorders, cancer, systemic lupus
 CC erythematosus or graft-versus-host disease; myeloid or lymphoid cell
 CC deficiencies; wound, burns, incisions and ulcers, osteoporosis or
 CC osteoarthritis; central and peripheral nervous system diseases and
 CC neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's
 CC disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;

CC haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis
 CC or systemic inflammatory response syndrome, ischaemia-reperfusion
 CC injury, endotoxin lethality, arthritis, inflammatory bowel disease or
 CC Crohn's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
 CC foliaceus.

XX Sequence 476 AA;

Query Match 99.4%; Score 2539; DB 23; Length 476;

Best Local Similarity 99.2%; Pred. No. 2.2e-240;

Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MYGAMMKVIVSLVLLMPGCDGLFHSLYRSVSMPPKSGDGLFPTPIYIAGKIQKREL 60

DB 1 MYGAMMKVIVSLVLLMPGCDGLFHSLYRSVSMPPKSGDGLFPTPIYIAGKIQKREL 60

QY 61 SLVGGPPGLNPKSYAGFLTVNKTYSNLFVWFPPAQIOPEDAPVVLWLQGGPGSSMFGL 120

DB 61 SLVGGPPGLNPKSYAGFLTVNKTYSNLFVWFPPAQIOPEDAPVVLWLQGGPGSSMFGL 120

QY 121 FVEHGPVVTSMNTLDRDRFPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180

DB 121 FVEHGPVVTSMNTLDRDRFPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180

QY 181 SALIOFFQIFPEYKKNDFVVTGESVAGKYVPAIAHLIHSNLPVREVKNLNGIAIGDYS 240

DB 181 SALIOFFQIFPEYKKNDFVVTGESVAGKYVPAIAHLIHSNLPVREVKNLNGIAIGDYS 240

QY 241 DPESIIIGGYAEFLYQIGLLDEKQKQYFQKQCEHIEHIRKQNWFEAFELDKLLDGLTFS 300

DB 241 DPESIIIGGYAEFLYQIGLLDEKQKQYFQKQCEHIEHIRKQNWFEAFELDKLLDGLTFS 300

QY 301 DSYFQNVGTGCSNYNFLRCTEPEDQLYVVKFSLPEVROAIVHGNQTFNDGTIVEKYLR 360

DB 301 DSYFQNVGTGCSNYNFLRCTEPEDQLYVVKFSLPEVROAIVHGNQTFNDGTIVEKYLR 360

QY 361 EDTVQSVKFWLTEIMNNYKVLINGQLDIIIVAAALTEISLMGMDWKSGOEYKKAQKWK 420

DB 361 EDTVQSVKFWLTEIMNNYKVLINGQLDIIIVAAALTEISLMGMDWKSGOEYKKAQKWK 420

QY 421 IPKSDSEVAGYIRQVDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

DB 421 IPKSDSEVAGYIRQVDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

RESULT 5

AAV13372

ID AAY13372 standard; Protein; 476 AA.

XX AC AAY13372;

XX DT 25-JUN-1999 (first entry)

XX DE Amino acid sequence of protein PRO223.

XX Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair.

XX OS Homo sapiens.

XX PN WO9914328-A2.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US19330.

XX PR 25-NOV-1997; 97US-0066840.

XX PR 17-SEP-1997; 97US-0059113.

PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 11; Fig 410; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX Sequence 476 AA;

Query Match 99.4%; Score 2538; DB 22; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-240;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQGLFLTPYIAGKIQKREL 60
DB 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQGLFLTPYIAGKIQKREL 60
QY 61 SLVGPPFGLNKMYSAGFLTVNKTNSNLFVFPFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
DB 61 SLVGPPFGLNKMYSAGFLTVNKTNSNLFVFPFPAQIQPEDAPVVLWLOGGPGSSMXGL 120
QY 121 FVEHGPFVYVTSNMTRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
DB 121 FVEHGPFVYVTSNMTRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIQFQIOPFPEYKNDFFVTGSEYAGKVPAIAHLIHSINPVRVKNLNGIAIGDGY 240
DB 181 SALIQFQIOPFPEYKNDFFVTGSEYAGKVPAIAHLIHSINPVRVKNLNGIAIGDGY 240
QY 241 DPESITGGVAFELYQIGLDEKOKYFQKOCHECIEHIRKQNFVFAFEILDKLLDGLTS 300
DB 241 DPESITGGVAFELYQIGLDEKOKYFQKOCHECIEHIRKQNFVFAFEILDKLLDGLTS 300
QY 301 DPSEYFQNVTCGSNNYFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR 360
DB 301 DPSEYFQNVTCGSNNYFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR 360
QY 361 EDTVQSVKVPWLTIMNNYKVLINGOLDIIVAAALTELSLGMWDWGSQYKAEKKVWK 420
DB 361 EDTVQSVKVPWLTIMNNYKVLINGOLDIIVAAALTELSLGMWDWGSQYKAEKKVWK 420
QY 421 IFKSDSEVAGYIRQVGDHGVIRGGGHILPYDQPLRAFPMINRFTYVGKWDVPYVG 476
DB 421 IFKSDSEVAGYIRQVGDHGVIRGGGHILPYDQPLRAFPMINRFTYVGKWDVPYVG 476

RESULT 8

AAB80240
ID AAB80240 standard; Protein; 476 AA.

XX AAB80240;

XX 24-APR-2001 (first entry)

XX Human PRO223 protein.

XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;

KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX ischaemia; inflammation.

OS Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 200WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0143698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski EJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

XX Williams PM, Wood WI;

XX WPI; 2001-081051/09.

XX N-PSDB; AAF72401.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -

XX Claim 1; Fig 60; 393pp; English.

XX The present sequence is one of sixty one novel secreted and

CC transmembrane PRO polypeptides. The PRO polypeptides are

CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung

CC squamous cell carcinoma), gastrointestinal disorders (e.g.

CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.

CC endometrial bleeding angiogenesis, ischaemias such as coronary

CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,

CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and

CC diabetes and retinal disorders such as retinitis pigmentosum.

CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 476 AA;

Query Match 99.4%; Score 2538; DB 22; Length 476;

Best Local Similarity 99.2%; Pred. No. 2.8e-240;

Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQGLFLTPYIAGKIQKREL 60

DB 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQGLFLTPYIAGKIQKREL 60

QY 61 SLVGPPFGLNKMYSAGFLTVNKTNSNLFVFPFPAQIQPEDAPVVLWLOGGPGSSMXGL 120

DB 61 SLVGPPFGLNKMYSAGFLTVNKTNSNLFVFPFPAQIQPEDAPVVLWLOGGPGSSMXGL 120

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NE, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-341586/32.
DR N-PSDB; ACA54942.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT or treating inflammatory diseases, organ failure, atherosclerosis,
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT Parkinson's disease -
XX
XX Claim 12; Fig 60; 473pp; English.
XX
XX The invention describes sixty one nucleic acids encoding PRO polypeptides
CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are
CC useful in diagnosing or treating enterocolitis, gastrointestinal
CC ulceration, skin diseases associated with abnormal keratinocyte
CC differentiation, e.g. psoriasis or epithelial cancers such as squamous
CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, AIDS, cancer,
CC diabetic complications, or mutations in general. The polypeptides are
CC also useful for wound repair and associated therapies concerned with
CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules
CC are also useful in gene therapy, and as molecular weight markers for
CC protein electrophoresis purposes. The anti-PRO antibodies may be used
CC in diagnostic assays for PRO, or for the affinity purification of PRO
CC from recombinant cell culture or natural sources. This is the amino
CC acid sequence of a novel human PRO polypeptide.
XX
SQ Sequence 476 AA;

Query Match 99.4%; Score 2538; DB 24; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-240;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMKVIIVSLVLLMPGCDGLFHSLSYRSVSPKPGDSQGLFPLPYIENGKIQKREL 60
DB 1 MVGAMKVIIVSLVLLMPGCDGLFHSLSYRSVSPKPGDSQGLFPLPYIENGKIQKREL 60
QY 61 SLVGPPFGLNKMKGAGFLTNKYNLFWFFPAQIQPEDAPVVLWLOGPGGSSMKGL 120
DB 61 SLVGPPFGLNKMKGAGFLTNKYNLFWFFPAQIQPEDAPVVLWLOGPGGSSMKGL 120
QY 121 FVEHGPVVTSSNMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
DB 121 FVEHGPVVTSSNMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
QY 181 SALIQFOIPEPKYNDFFYTGESYAGKYVPAIAHLIHSNLPVREKINLINGAIGDGVY 240
DB 181 SALIQFOIPEPKYNDFFYTGESYAGKYVPAIAHLIHSNLPVREKINLINGAIGDGVY 240
QY 241 DPSSIIGGYAEFLYIGLLDEKQKFKOCHIEHRIKONNFEAFIILDKLDDGLTS 300
DB 241 DPSSIIGGYAEFLYIGLLDEKQKFKOCHIEHRIKONNFEAFIILDKLDDGLTS 300
QY 301 DPSYFQNVTCGSNNYFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVVKYL 360
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QY 361 EDTVQSVKPLWTEIMNMYKVLINGQLDIIVAALATERSLGMGMDWGSQYKKAEEKVWK 420
DB 361 EDTVQSVKPLWTEIMNMYKVLINGQLDIIVAALATERSLGMGMDWGSQYKKAEEKVWK 420
QY 421 IFKSDSEVAGYIRQVGFHVIIRGGGHILPYDQPLRAFDMINRFYIKGWDPIYVG 476
DB 421 IFKSDSEVAGYIRQVGFHVIIRGGGHILPYDQPLRAFDMINRFYIKGWDPIYVG 476

RESULT 10
ABU71316
ID ABU71316 standard; Protein; 476 AA.
XX
XX AC ABU71316;
XX DT 10-JUN-2003 (first entry)
XX DE Human PRO223 protein.
XX KW Human; PRO; secreted; transmembrane; cytosolic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
XX differentiation; tumour; gene therapy.
XX OS Homo sapiens.
XX PN US2003036143-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-0187600.
XX PR 16-SEP-1998; 98WO-US19330.
XX PR 07-OCT-1998; 98WO-US21144.
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 14-MAY-1999; 99WO-US10733.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 02-DEC-1999; 99WO-US28551.
XX PR 30-DEC-1999; 99WO-US31274.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 24-FEB-2000; 2000WO-US05004.
XX PR 01-MAR-2000; 2000WO-US05601.
XX PR 02-MAR-2000; 2000WO-US05841.
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XX PR 02-JUN-2000; 2000WO-US15264.
XX PR 28-JUL-2000; 2000WO-US20710.
XX PR 24-AUG-2000; 2000WO-US23328.
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XX PR 20-JUN-2001; 2001WO-US19692.
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XX PR 09-JUL-2001; 2001WO-US21735.
XX PR 29-AUG-2001; 2001WO-US27099.
XX PR 18-SEP-1997; 97US-059263P.
XX PR 18-SEP-1997; 97US-059266P.
XX PR 17-OCT-1997; 97US-062250P.
XX PR 21-OCT-1997; 97US-063486P.
XX PR 24-OCT-1997; 97US-063120P.
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XX PR 13-NOV-1997; 97US-065311P.
XX PR 21-NOV-1997; 97US-066120P.
XX PR 24-NOV-1997; 97US-066466P.

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PR 11-DEC-1997; 97US-069335P.
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PR 02-SEP-1998; 98US-098821P.
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PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.
PR 10-SEP-1998; 98US-099812P.
Query Match 99.4%; Score 2538; DB 24; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-240;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MYGAMWKIVSLVLLMPPGCDGLFHSLYRSVSMPPKGDGSQLFTPTYEAGKIQKREL 60
Db 1 MYGAMWKIVSLVLLMPPGCDGLFHSLYRSVSMPPKGDGSQLFTPTYEAGKIQKREL 60
Qy 61 SLVGGPPGLNKMKSAGFLTVNKTYSNLFVFFPPAQIQEPEDAPVVLWLOGGPGSSMXGL 120
Db 61 SLVGGPPGLNKMKSAGFLTVNKTYSNLFVFFPPAQIQEPEDAPVVLWLOGGPGSSMXGL 120
Qy 121 FVEHGPVVTSNNTLRDRFPWTTTXXSMLYINDPVGTSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTSNNTLRDRFPWTTTXXSMLYINDPVGTSFTDDTHGYAVNEDDVARDLY 180
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Dd	241	DPESI IGGYA EFL YQIGLLDEKQKY FOKQCHECIEHIRKQNWFEAF EILDKLDGDLTS	300
Qy	301	DPSEY FONVTCGS NYNLFLECTEPEDOLYYVKFSL PEVRQA IHVGNOTFNDGTIVEKYLR	360
Dd	301	DPSEY FONVTCGS NYNLFLECTEPEDOLYYVKFSL PEVRQA IHVGNOTFNDGTIVEKYLR	360
Qy	361	EDTVQS VKPWL TEIMNNYKVLYINGQLDII VAAAL TERSLMGM DWKGSQEYKKA EKKWVK	420
Dd	361	EDTVQS VKPWL TEIMNNYKVLYINGQLDII VAAAL TERSLMGM DWKGSQEYKKA EKKWVK	420
Qy	421	IFKSDSEVAGYIRQGDGHQVIIRGGGHILPYDQPLRAFDMINRFYKGWDPIVG	476
Dd	421	IFKSDSEVAGYIRQGDGHQVIIRGGGHILPYDQPLRAFDMINRFYKGWDPIVG	476

RESULT 11
ABU71473
ID ABU71473 standard; Protein; 476 AA.
XX
AC AC
ABU71473;
XX XX
DATE 30 JUN 2002 /6194267473/

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PR 24-OCT-1997; 97US-062816P.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX PI Pilvaroff E, Pong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Klijavin ID;
XX PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX PI Williams PM, Wood WI;
XX WPI: 2003-361832/34.
XX N-PSDB; AC358427.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
XX PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
XX PT generating antisense RNA and DNA, and in gene therapy -
XX PT
XX Claim 12; Fig 60; 474pp; English.
XX
XX The present invention relates to the isolation of novel human secreted
XX CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
XX CC sequences encoding them. The polynucleotide sequences are useful in
XX CC molecular biology, as hybridisation probes, in chromosome and gene
XX CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
XX CC polynucleotide sequences may also be used in preparing PRO polypeptides
XX CC by recombinant techniques, and in generating either transgenic animals
XX CC or knock-out animals which, in turn, are useful in the development and
XX CC screening of therapeutically useful reagents. The PRO polypeptides or
XX CC their antibodies are useful in preparing a medicament for treating a
XX CC condition responsive to the polypeptide or antibody, such as cancer,
XX CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
XX CC ABU71445-ABU71505 represent human PRO polypeptides of the invention.
XX
XX Sequence 476 AA;
XX
XX Query Match 99.4%; Score 2538; DB 24; Length 476;
XX Best Local Similarity 99.2%; Pred. NO. 2.8e-240;
XX Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSNPPKGDGQPLFLTPYIEAGKIQKREL 60
XX DB 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSNPPKGDGQPLFLTPYIEAGKIQKREL 60
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XX QY 61 SLVGPPFGLNMKSYAGFLTVNKTYSNLNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMXGL 120
XX DB 61 SLVGPPFGLNMKSYAGFLTVNKTYSNLNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMXGL 120
XX
XX QY 121 FVEHGYVVTNNLTDRDPFWTTTYSMLYIDNPVGTGSGFTDTHGYAVNEDDVARDLY 180
XX DB 121 FVEHGYVVTNNLTDRDPFWTTTYSMLYIDNPVGTGSGFTDTHGYAVNEDDVARDLY 180
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XX DB 181 SALIQFQFIPPEYKNNDFVYTGSGYAGKVVPATLHLSNPVREKINLNGTAIGDGY 240
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XX QY 241 DPESIIGGYAEFLYQIGLDEKQKFKQKQCECIEHIRKQNNFEAFEILDKLDGDLTS 300
XX DB 241 DPESIIGGYAEFLYQIGLDEKQKFKQKQCECIEHIRKQNNFEAFEILDKLDGDLTS 300
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XX QY 301 DPSYFQNTGCSNYNPLRCTEPEDQIYYVKFTSLPEVROAIHVGNQTFNDGTIVEKYLR 360
XX DB 301 DPSYFQNTGCSNYNPLRCTEPEDQIYYVKFTSLPEVROAIHVGNQTFNDGTIVEKYLR 360
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XX DB 361 EDTVQSVKPKWLTEIMNNYKVLIVNGOLDIIVAAALTERSLMGMDWKGSGQYKAEKKVWK 420
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XX QY 421 IFKSDSEVAGYIRQVGDHFQVIIRGGGHILPYDQPLRAFDMINRFYIGKGMDDPYVG 476
XX DB 421 IFKSDSEVAGYIRQVGDHFQVIIRGGGHILPYDQPLRAFDMINRFYIGKGMDDPYVG 476
XX
XX RESULT 12

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RESULT 12

ABU71919
ID ABU71919 standard; Protein; 476 AA.
XX
AC ABU71919;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO223.
XX
XX Human; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker.
XX Homo sapiens.
OS
XX
FN US2003003530-A1.
XX
PD 02-JAN-2003.
XX
PF 11-JUL-2001; 2001US-0904011.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
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PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
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PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 17-SEP-1997; 97US-059113P.
PR 17-SEP-1997; 97US-059115P.
PR 17-SEP-1997; 97US-059117P.
PR 17-SEP-1997; 97US-059119P.
PR 17-SEP-1997; 97US-059121P.
PR 17-SEP-1997; 97US-059122P.
PR 17-SEP-1997; 97US-059124P.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063045P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 24-OCT-1997; 97US-063127P.
PR 24-OCT-1997; 97US-063128P.
PR 27-OCT-1997; 97US-063327P.
PR 27-OCT-1997; 97US-063329P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063542P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063549P.
PR 28-OCT-1997; 97US-063550P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-063704P.
PR 29-OCT-1997; 97US-063732P.
PR 29-OCT-1997; 97US-063734P.
PR 29-OCT-1997; 97US-063735P.
PR 29-OCT-1997; 97US-063738P.
PR 29-OCT-1997; 97US-064215P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 03-NOV-1997; 97US-064248P.
PR 07-NOV-1997; 97US-064809P.
PR 12-NOV-1997; 97US-065186P.
PR 17-NOV-1997; 97US-065846P.
PR 18-NOV-1997; 97US-065693P.
PR 21-NOV-1997; 97US-066120P.
PR 21-NOV-1997; 97US-066364P.
PR 24-NOV-1997; 97US-066453P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066511P.
PR 24-NOV-1997; 97US-066770P.
PR 24-NOV-1997; 97US-066772P.
PR 18-SEP-2000; 2000US-0665350.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N,
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini Iu;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-329602/31.
XX N-PSDB; ACR60134.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, in generating probes and in tissue typing -
XX
XX Claim 12; Fig 60; 484pp; English.
XX
XX The invention relates to an isolated nucleic acid with at least 80%
CC nucleic acid sequence identity to a nucleotide sequence encoding one of
CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
CC PRO protein extracellular domain. Also included are a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity
CC to: (a) an amino acid sequence selected from the 61 PRO proteins;
CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited
CC with an ATCC number (detailed in the specification); or (c) an
CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking
CC its associated signal peptide), a chimeric molecule comprising a PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO245 or PRO1868 in a sample suspected of
CC containing the polypeptide, linking a bioactive molecule to a cell
CC expressing a PRO245 or PRO1868 and modulating at least one biological
CC activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which
CC encode PRO can be used to generate either transgenic animals or knock-out
CC animals which may be used in the development and screening of
CC therapeutically useful reagents. The nucleic acids may also be used in
CC gene therapy, in chromosome identification, as chromosome markers, or in
CC generating probes. The PRO polypeptides are useful as molecular markers
CC for protein electrophoresis, and the isolated nucleic acids may be used
CC for recombinantly expressing those markers. The PRO polypeptides and
CC nucleic acids may also be used in tissue typing. Anti-PRO antibodies
CC are useful in diagnostic assays for PRO, and in affinity purification
CC of PRO from recombinant cell culture or natural sources. The
CC present sequence represents a PRO protein.

RESULT 13

PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084633P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087603P.
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PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
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PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
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PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
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PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
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PR 01-JUL-1998; 98US-091359P.
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PR 02-JUL-1998; 98US-091478P.
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PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.

PR 10-AUG-1998; 98US-095998P.
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PR 17-AUG-1998; 98US-096757P.
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PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 26-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 01-SEP-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 02-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.

Query Match 99.4%; Score 2538; DB 24; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-240;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 1 MYGAMMKVIVSLVLLMPGCDGLFHSLYRSVSMPPKSGDGLFLTPYIEAGKIQKREL 60

QY 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFVWFPPAQIQPEDAPVVLWLOGGPGSSMGL 120
DB 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFVWFPPAQIQPEDAPVVLWLOGGPGSSMGL 120

QY 121 FVEHGPVVTNMTLRDRDPWTTTSMLYINDVPYGTGFTDDTHGYAVNDDVARDLY 180
DB 121 FVEHGPVVTNMTLRDRDPWTTTSMLYINDVPYGTGFTDDTHGYAVNDDVARDLY 180

QY 181 SALIOFFQIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSNFPVREYKINLNGIAIGDGYS 240
DB 181 SALIOFFQIFPEYKQNDFFVTGSEYAGKYVPAIAHLIHSNFPVREYKINLNGIAIGDGYS 240

QY 241 DPESIIGGYAEFLYQIGLLDEKQKQYFQKQCHCEHIEHIRKQNWFEAFELDKLLDGLTS 300
DB 241 DPESIIGGYAEFLYQIGLLDEKQKQYFQKQCHCEHIEHIRKQNWFEAFELDKLLDGLTS 300

QY 301 DPSYFQNTGCSNYNFLRCTEPEDQLYYVKFSLPEVROAIVHGNQTFNDGTIVKYLUR 360
DB 301 DPSYFQNTGCSNYNFLRCTEPEDQLYYVKFSLPEVROAIVHGNQTFNDGTIVKYLUR 360

QY 361 EDTVQSVKPELTEMNNYKVLIIYNGQLDIIAAALTEFLSMGMWKGSGEYKKAEEKVWK 420
DB 361 EDTVQSVKPELTEMNNYKVLIIYNGQLDIIAAALTEFLSMGMWKGSGEYKKAEEKVWK 420

QY 421 IPKSDSEVAGYIRQGDHFHQVIRGGGHILPYDQPLRAFDMNIRFYKGGWDPYVG 476
DB 421 IPKSDSEVAGYIRQGDHFHQVIRGGGHILPYDQPLRAFDMNIRFYKGGWDPYVG 476

RESULT 14
ABU66106
ID ABU66106 standard; Protein; 476 AA.
XX
AC ABU66106;
XX
DT 20-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO223.
XX
KW Human; secreted protein; transmembrane protein; cytostatic;
KW gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

XX US2003036157-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-0188769.

XX 16-SEP-1998; 98WO-US19330.

XX 07-OCT-1998; 98WO-US21141.

XX 01-DEC-1998; 98WO-US25108.

XX 08-MAR-1999; 99WO-US05028.

XX 14-MAY-1999; 99WO-US10733.

XX 02-JUN-1999; 99WO-US12252.

XX 01-SEP-1999; 99WO-US20111.

XX 15-SEP-1999; 99WO-US21090.

XX 01-DEC-1999; 99WO-US28301.

XX 02-DEC-1999; 99WO-US28551.

XX 30-DEC-1999; 99WO-US31374.

XX 05-JAN-2000; 2000WO-US00219.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US05004.

XX 01-MAR-2000; 2000WO-US05501.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 30-MAR-2000; 2000WO-US08439.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

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XX 02-JUN-2000; 2000WO-US15264.

XX 28-JUL-2000; 2000WO-US20710.

XX 24-AUG-2000; 2000WO-US23328.

XX 08-NOV-2000; 2000WO-US30952.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000WO-US34956.

XX 28-FEB-2001; 2001WO-US06520.

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XX 09-JUL-2001; 2001WO-US21735.

XX 29-AUG-2001; 2001WO-US27099.

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27-MAR-1998;

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24-JUN-1998;

24-JUN-1998;

CC	gene therapy. The polynucleotide may also be used in preparing PRO
CC	polypeptides by recombinant techniques, and in generating either
CC	transgenic animals or knock-out animals which, in turn, are useful in the
CC	development and screening of therapeutically useful reagents. The PRO
CC	polypeptide or the antibody is used in preparing a medicament for
CC	treating a condition responsive to the polypeptide or antibody, such as
CC	mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC	psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC	e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC	atrophia areata, angiogenesis, inflammatory disease e.g asthma and
CC	rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC	present sequence represents the amino acid sequence of a PRO polypeptide.
XX	
SQ	Sequence 476 AA;
	Query Match 99.4%; Score 2538; DB 24; Length 476;
	Best Local Similarity 99.2%; Pred. No. 2.8e-240;
	Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 MYGAMWKIVISLVILMPGPCDGLFHSLYRSVSMPPKGDGSQLFLTPYIEAGKIQGREL 60
Dd	1 MYGAMWKIVISLVILMPGPCDGLFRSLYSVSMPPKGDGSQLFLTPYIEAGKIQGREL 60
Qy	61 SLVGPPFPGLNKMKS YAGFLT VANKT YNSNL FFWFFPAQIQPEDAPVVLWLOGPGGSNMXGL 120
Dd	61 SLVGPPFPGLNKMKS YAGFLT VANKT YNSNL FFWFFPAQIQPEDAPVVLWLOGPGGSNMFGI 120
Qy	121 FVEHGPVVYVTSNMTLRDRDFPWTXTXSMLYIDNPVGTGPFSTDDTHGYAVNEEDVDARDLY 180
Dd	121 FVEHGPVVYVTSNMTLRDRDFPWTTL SMLYIDNPVGTGFSFTDDTHGYAVNEEDVDARDLY 180
Qy	181 SALIOFFQIFPEYKKNDFPVVTGESYAGKYVPDAIAHLIHSLNPREVKINLNGTAIGDGYS 240
Dd	181 SALIOFFQIFPEYKKNDFPVVTGESYAGKYVPDAIAHLIHSLNPREVKINLNGTAIGDGYS 240
Qy	241 DPESIIGGAAYEFLYQIGLLDEKQKXYFOKECHEIEHIRKQNWFEPFEILLKLDDGLTS 300
Dd	241 DPESIIGGAAYEFLYQIGLLDEKQKXYFOKECHEIEHIRKQNWFEPFEILLKLDDGLTS 300
Qy	301 DPSYFONVTGCSSNYNFRLRCTEPEDQLYYVVFSLPEVRQA IHVGNQTFNDGTIVEKYLR 360
Dd	301 DPSYFONVTGCSSNYNFRLRCTEPEDQLYYVVFSLPEVRQA IHVGNQTFNDGTIVEKYLR 360
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Dd	361 EDTVQSVPKWLTEIMNNYKVLIYNGOLD I IVAAL TERSLMGMWDKWSQEYKKAEEKVWK 420
Qy	421 IFKSDSEVAGYIRQVGFHQVIIRGGGHILPYDQPLRAFDMINRFYIKGWDPYVG 476
Dd	421 IFKSDSEVAGYIPQAGDHQHWITGGCHI I PYDQPLRAFDMINRFYIKGWDPYVG 476

Search completed: November 7, 2003, 16:43:01
Job time : 51 secs

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R	21-OCT-1997;	97US-063486P.	
R	24-OCT-1997;	97US-062814P.	
R	24-OCT-1997;	97US-062816P.	
R	24-OCT-1997;	97US-063045P.	
R	24-OCT-1997;	97US-063120P.	
R	24-OCT-1997;	97US-063121P.	
R	24-OCT-1997;	97US-063127P.	
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R	27-OCT-1997;	97US-063329P.	
R	28-OCT-1997;	97US-063541P.	
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R	28-OCT-1997;	97US-063564P.	
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R	29-OCT-1997;	97US-063732P.	
R	29-OCT-1997;	97US-063734P.	
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R	31-OCT-1997;	97US-063870P.	
R	31-OCT-1997;	97US-064103P.	
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R	07-NOV-1997;	97US-064809P.	
R	12-NOV-1997;	97US-065186P.	
R	17-NOV-1997;	97US-065846P.	
R	18-NOV-1997;	97US-065693P.	
R	21-NOV-1997;	97US-066120P.	
R	21-NOV-1997;	97US-066364P.	
R	24-NOV-1997;	97US-066453P.	
R	24-NOV-1997;	97US-066466P.	
R	24-NOV-1997;	97US-066511P.	
R	24-NOV-1997;	97US-066770P.	
R	24-NOV-1997;	97US-066772P.	
R	25-NOV-1997;	97US-066840P.	
R	12-DEC-1997;	97US-069425P.	
R	04-JUN-1998;	98US-088026P.	
R	10-SEP-1998;	98US-099803P.	
R	14-SEP-1998;	98US-100262P.	
R	17-SEP-1998;	98US-100858P.	
R	13-OCT-1998;	98US-104080P.	
R	20-NOV-1998;	98US-109304P.	
R	22-DEC-1998;	98US-113296P.	
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R	26-JUL-1999;	99US-145698P.	
R	28-JUL-1999;	99US-146222P.	
R	18-SEP-2000;	2000US-0665350.	
(GETH) GENENTECH INC.			
A	Ashtkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;		
X	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;		
I	Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;		
I	Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;		
I	Williams PM, Wood WI;		
X	WPI; 2003-331485/31.		
X	N-PSDB: ACA05472		

Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1869, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease - Example 27; Fig 60; 481pp; English.

The invention relates to sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in

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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:42:09 ; Search time 21 Seconds
(without alignments)
959.046 Million cell updates/sec

Title: US-10-084-018-3
Perfect score: 2554
Sequence: 1 MVGAMKWKIVSLVLLMPGPC.....RAFDMINRFYKGDWDPYVG 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550	99.8	476	2	US-08-828-488-3
2	2550	99.8	476	4	US-09-299-689A-3
3	2512.5	98.4	477	2	US-08-828-488-1
4	2512.5	98.4	477	4	US-09-299-689A-1
5	1772.5	69.4	351	2	US-08-828-488-5
6	1772.5	69.4	351	4	US-09-299-689A-5
7	1014	39.7	471	2	US-08-828-488-7
8	1014	39.7	471	4	US-09-299-689A-7
9	557	21.8	480	2	US-08-828-488-8
10	557	21.8	480	4	US-09-299-689A-8
11	557	21.8	480	4	US-09-702-705-336
12	557	21.8	480	4	US-09-736-457-336
13	498.5	19.5	491	1	US-09-640-305-4
14	498.5	19.5	491	1	US-08-360-673-4
15	472.5	18.5	557	1	US-08-309-341-2
16	472.5	18.5	557	1	US-08-608-267-2
17	472.5	18.5	557	1	US-08-608-452-2
18	472.5	18.5	557	1	US-08-608-224-2
19	472.5	18.5	557	2	US-08-967-149-2
20	455.5	17.8	557	1	US-08-309-341-4
21	455.5	17.8	557	1	US-08-608-267-4
22	455.5	17.8	557	1	US-08-608-452-4
23	455.5	17.8	557	1	US-08-608-224-4
24	455.5	17.8	557	2	US-08-967-149-4
25	432	16.9	532	2	US-08-899-324-33
26	432	16.9	532	3	US-08-329-892B-33
27	427	16.7	421	2	US-08-807-263-4

Query Match 99.8%; Score 2550; DB 2; Length 476;

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29 361 14.1 554 3 US-08-943-714-2
30 352 13.8 446 1 US-08-665-966-10
31 352 13.8 446 3 US-09-041-780-10
32 330.5 12.9 523 3 US-08-943-714-11
33 299.5 11.7 481 3 US-08-943-714-10
34 278 10.9 530 3 US-08-943-714-12
35 235 9.2 179 1 US-08-665-966-8
36 235 9.2 179 3 US-09-041-780-8
37 103 4.0 2548 4 US-09-172-422-1
38 102 4.0 622 2 US-08-664-646A-2
39 102 4.0 622 2 US-09-066-285-2
40 102 4.0 622 3 US-09-261-006-2
41 102 4.0 622 3 US-08-951-088-2
42 102 4.0 622 4 US-09-609-566-2
43 102 4.0 622 4 US-09-609-570-2
44 102 4.0 622 4 US-09-427-372-2
45 102 4.0 622 4 US-09-693-554-2

ALIGNMENTS

RESULT 1
US-08-828-488-3
; Sequence 3, Application US/08828488
; Patent No. 592521
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,488
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MMLR3DT01
; CLONE: 566993

US-08-828-488-3

Best Local Similarity 100.0%; Pred. No. 1e-259;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SLVGPPFGLNKSAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGGSGSMXGL 120
QY 121 FVEHGPVYVTSNMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
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QY 181 SALIQFOIFPEYKNDPVTGSGYAGKYVPAIAHLIHSNLPREVKNLNGIAIGDGY 240
DB 181 SALIQFOIFPEYKNDPVTGSGYAGKYVPAIAHLIHSNLPREVKNLNGIAIGDGY 240
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DB 361 EDTVQSVKPLTEIMNNYKVLINYLINGQDIIIVAAALTSRLMGMDWKGQYKKAQKVK 420
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DB 421 IFKSDSEVAGYIRQVGFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

RESULT 2

US-09-299-689A-3
; Sequence 3, Application US/09299689A
; Patent No. 6379913
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,689A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,488
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MMLRJD01
; CLONE: 566993
US-09-299-689A-3

Query Match 99.8%; Score 2550; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1e-259;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGAMWKVIVSLVLLMPGCDGLFHSLSYRSVSMPPKSGDGLFLTPYIEAGKIQKREL 60
DB 1 MVGAMWKVIVSLVLLMPGCDGLFHSLSYRSVSMPPKSGDGLFLTPYIEAGKIQKREL 60
QY 61 SLVGPPFGLNKSAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGGSGSMXGL 120
DB 61 SLVGPPFGLNKSAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGGSGSMXGL 120
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DB 121 FVEHGPVYVTSNMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
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DB 181 SALIQFOIFPEYKNDPVTGSGYAGKYVPAIAHLIHSNLPREVKNLNGIAIGDGY 240
QY 241 DPESIIGYAEFLYQIGLLDEKQKYFOKQCHECHIEHIRKQNWFEAFELDKLLDGLTS 300
DB 241 DPESIIGYAEFLYQIGLLDEKQKYFOKQCHECHIEHIRKQNWFEAFELDKLLDGLTS 300
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DB 301 DPYSFQNVTCGSNYNFLRCTEPEDQLYYVKFSLPEVROAIHVGNOTFNDGTIVEKYLR 360
QY 361 EDTVQSVKPLTEIMNNYKVLINYLINGQDIIIVAAALTSRLMGMDWKGQYKKAQKVK 420
DB 361 EDTVQSVKPLTEIMNNYKVLINYLINGQDIIIVAAALTSRLMGMDWKGQYKKAQKVK 420
QY 421 IFKSDSEVAGYIRQVGFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476
DB 421 IFKSDSEVAGYIRQVGFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

RESULT 3

US-08-828-488-1
; Sequence 1, Application US/0828488
; Patent No. 5925521
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,488
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0241 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPHGNOT03
CLONE: 443004

US-08-828-488-1

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RESULT 4

US-09-299-689A-1
Sequence 1, Application US/09299689A
Patent No. 6379913
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SERINE

TITLE OF INVENTION: CARBOXYPEPTIDASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,689A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,488
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0241 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPHGNOT03
CLONE: 443004

US-09-299-689A-1

Query Match 98.4%; Score 2512.5; DB 4; Length 477;
Best Local Similarity 98.5%; Pred. No. 9e-256;
Matches 470; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 MVGAMKVIUSLVLLMPGCDGLFHSLYRSVSMPPKGDSCQPLFLTPYEAGKIQGREL 60
DB 1 MVGAMKVIUSLVLLMPGCDGLFHSLYRSVSMPPKGDSCQPLFLTPYEAGKIQGREL 60
QY 61 SLVGPPPLNKMKS YAGELTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGGSGSMXGL 120
DB 61 SLVGPPPLNKMKS YADFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGGSGSMFGL 120
QY 121 FVEHGPYVVTSSNMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
DB 121 FVEHGPYVVTSSNMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIQFQIIPFYKXNDFFVTGSEYAGKYVPAIAHLIHSNPVREVKNLNGIAIGDGS 240
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DB 301 DPSEYFQNTGCSNYNFLRCTEPEPDLQYVVKFSLPEVRQAIHVGNQTFNDGTIVEKYL 360
QY 361 EDTVQSVKPMWLTETMNNYKVLINYGOLDIIVAAALTEKSLMGMDWKGSGQYKAE-KKW 419
DB 361 EDTVQSVKPMWLTETMNNYKVLINYGOLDIIVAAALTEKSLMGMDWKGSGQYKAEKKW 420
QY 420 KIFKSDSEVAGYIROVGDPHQVIRGGGHILPYDQPLRAFDNIRFIYKGGWDPYVG 476
DB 421 KIFKSDSGVAGYIROVGDPHQVIRGGGHILPYDQPLRAFDNIRFIYKGGWDPYVG 477

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RESULT 5
US-08-828-488-5
; Sequence 5, Application US/08828488
; Patent No. 5925521
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,488
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNCR01
; CLONE: 770469
;
US-08-828-488-5
Query Match 69.4%; Score 1772.5; DB 2; Length 351;
Best Local Similarity 72.7%; Pred. No. 5e-178;
Matches 346; Conservative 2; Mismatches 3; Indels 125; Gaps 2;

QY 1 MVGAMWKVIVSLVLLMPGCDGLPHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPGCDGLPHSLYRSVSMPPKGDGQPLFLTPYIEAGKI----- 54
QY 61 SLVGFPFGLNKMKS YAGFLTVNKTYSNLF FFFPAQIQPEDAPVVLWLOGGPGGSSMXGL 120
Db 55 ----- 54
QY 121 FVEHGPVVTNSMTLRDRDPFWTTXSMLYIDNPVGTGFSTDDTHGYAVNEDDVARDLY 180
Db 55 -----YTGTNSV----- 61
QY 181 SALIQFOIPEYKNDPVYTGESYAGKYVPATAHLTHSLNPVREVKNLNGTAIGDYS 240
Db 62 -----FOIPEYKNDPVYTGESYAGKYVPATAHLTHSLNPVREVKNLNGTAIGDYS 115
QY 241 DPESIIGGYAEFLYQIGLLDEKOKYFQKQCHIEHIRKQNWFEAFEILDKLLDGLTS 300
Db 1 DPESIIGGYAEFLYQIGLLDEKOKYFQKQCHIEHIRKQNWFEAFEILDKLLDGLTS 175
QY 301 DPSEYFQNTGCSNYNFLRCTEPEDQLYYVKFSLPEVRQAIVHVGNTFDGTIVEKYLR 360
Db 176 DPSEYFQNTGCSNYNFLRCTEPEDQLYYVKFSLPEVRQAIVHVGNTFDGTIVEKYLR 235
QY 361 EDTVQSVKPELWTEIMNNYKVLINYGOLDIIVAAALTEKSLMGMDWKGSOEYKKAEEKVWK 420
Db 236 EDTVQSVKPELWTEIMNNYKVLINYGOLDIIVAAALTEKSLMGMDWKGSOEYKKAEEKVWK 295
QY 421 IFKSDSEVAGYIRQVGDHFQVIRGGGHILPYDQPLRAFDMINRPIYKGGWDPYVG 476
Db 296 IFKSDSEVAGYIRQVGDHFQVIRGGGHILPYDQPLRAFDMINRPIYKGGWDPYVG 351

RESULT 6
US-09-299-689A-5
; Sequence 5, Application US/09299689A
; Patent No. 6379913
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,689A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,488
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNCR01
; CLONE: 770469
;
US-09-299-689A-5
Query Match 69.4%; Score 1772.5; DB 4; Length 351;
Best Local Similarity 72.7%; Pred. No. 5e-178;
Matches 346; Conservative 2; Mismatches 3; Indels 125; Gaps 2;

QY 1 MVGAMWKVIVSLVLLMPGCDGLPHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPGCDGLPHSLYRSVSMPPKGDGQPLFLTPYIEAGKI----- 54
QY 61 SLVGFPFGLNKMKS YAGFLTVNKTYSNLF FFFPAQIQPEDAPVVLWLOGGPGGSSMXGL 120
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Db 55 ----- 54
QY 121 FVEHGPVVTSMNLTDRDPFTTSMXYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 55 -----YGTNSV----- 61
QY 181 SALIQFQIPPEYKNNDFYVTGSGYAGKYPAIAHLIHSNPNREVKNINLNGAIGDYS 240
Db 62 -----FOIPPEYKNNDFYVTGSGYAGKYPAIAHLIHSNPNREVKNINLNGAIGDYS 115
QY 241 DPESIIIGGYAEFLYQIGLLDEKQKYYFQKQCHIEHIRKQNFPEAFIILDKLLDGLTS 300
Db 116 DPESIIIGGYAEFLYQIGLLDEKQKYYFQKQCHIEHIRKQNFPEAFIILDKLLDGLTS 175
QY 301 DPYFQNVTCGSNNYFNLCRTEPDQLYYKFLSLPEVROAIHVGNOTFNDGTIVEKYL 360
Db 176 DPYFQNVTCGSNNYFNLCRTEPDQLYYKFLSLPEVROAIHVGNOTFNDGTIVEKYL 235
QY 361 EDTVQSVKPLTEIMNNYKVLINYGQDIIIVAAALTEKSLMGDMWKGQSYKKAQKVK 420
Db 236 EDTVQSVKPLTEIMNNYKVLINYGQDIIIVAAALTEKSLMGDMWKGQSYKKAQKVK 295
QY 421 IFKSDSEVAGYIROVGFHVIIRGGHILPYDQPLAFDMINRFIYKGMWDPVVG 476
Db 296 IFKSDSEVAGYIROVGFHVIIRGGHILPYDQPLAFDMINRFIYKGMWDPVVG 351

RESULT 7
US-08-828-488-7
; Sequence 7, Application US/08828488
; Patent No. 5925521
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,488
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

; LIBRARY: GenBank
; CLONE: 1718107
; US-08-828-488-7
Query Match 39.7%; Score 1014; DB 2; Length 471;
Best Local Similarity 43.9%; Pred No. 6 4e-98;
Matches 197; Conservative 95; Mismatches 145; Indels 12; Gaps 7;
QY 24 FHSLYRSVMPK-GDSGQPLFTTYEAGKIQKRELSLVGFFPGLNKMKSAGFTVVK 82
Db 26 YKLMRGSASPPRGESGEPFLTLLQDGKTEBARKARVNHMLSSVESYSGFTVDA 85
QY 83 TYSNLFVFFFAQIQPEDAPVVLWLOGSPGSSMXGLFVEHGPVVTSMNLTDRDPFW 142
Db 86 KNSNLFVFPVPAKNNREQAPILWLOGGPGASSLFGMFEENGPFPHIRKNSYKQREYSW 145
QY 143 TTTXSNLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFQIPPEYKNNDFYVTG 202
Db 146 HQNHMIYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFQIPPEYKNNDFYVTG 205
QY 203 ESYAGKYVPAIAHLIHSNPNREVKNINLNGAIGDYSDPESIIGGYAEFLYQIGLLDEK 262
Db 206 ESYAGKYVPAIAHLIHSNPNREVKNINLNGAIGDYSDPESIIGGYAEFLYQIGLLDEK 262
QY 263 QKYYFQKQCHIEHIRKQNFPEAFIILDKLLDGLTSDPYFQNVTCGSNNYFNLCRTE 322
Db 263 GRKFDDEDATAAIAACAEKMDMSANRLIQGLFDG-LDGOESYFKKVTGFSYFNFKGDE 321
QY 323 PEDQ-LYYVVFSLPEVROAIHVGNOTFNDG--TIVEKYLREDTQSVKPLTEIMNNY 378
Db 322 ESKQDSVLMFSLNPNREVKNINLNGAIGDYSDPESIIGGYAEFLYQIGLLDEK 381
QY 379 KVLINYGQDIIIVAAALTEKSLMGDMWKGQSYKKAQKVKIFKSDSEVAGYIROVGF 438
Db 382 RVLFYNGQDIIIVAAALTEKSLMGDMWKGQSYKKAQKVKIFKSDSEVAGYIROVGF 438
QY 439 HQVIRGGHILPYDQPLAFDMINRFIY 467
Db 439 QEVLIIRNAGHVMVRDQPKWAFDMITSFTH 467

RESULT 8
US-09-299-689A-7
; Sequence 7, Application US/09299689A
; Patent No. 6379913
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,689A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,488
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

/ Sequence 8, Application US/09299689A
/ Patent No. 6379913
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Hawkins, Phillip R.
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Goli, Surya K.
/ TITLE OF INVENTION: NOVEL HUMAN SERINE
/ CARBOXYPEPTIDASE
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA: US/09/299,689A
/ APPLICATION NUMBER: 08/828,488
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0241 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 480 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 190283
/ US-09-299-689A-8

Query Match 21.8%; Score 557; DB 4; Length 480;
Best Local Similarity 28.0%; Pred. No. 9.2e-50;
Matches 148; Conservative 91; Mismatches 162; Indels 128; Gaps 20;
QY 12 LVLMPGCDGLFHSLSYRSVMPKGDGQPLFLTPYIEAGKIQKRELSLVGPFPL-- 69
DB 1 MIRAAPPFLFLLLLLLLVSWASRGEAAP-----DQDETQR-----LPLAK 43
QY 70 --NMKSAGFLTVNKTNSNLPFWFPFPAIQPEDAPVVLWLOGGPGSSMXGLFVEHGPY 127
DB 44 QPSFRQYSGYL--KSSGSKHLHYWFVESQKDPNSPVVLWNGGPGCSSLDGLLTHGPF 101
QY 128 VV-TSNMTLRDRDPFWTTXSMLYIDNPVGTGFTDTHGYAVNEDDVARLDYLSALIQF 186
DB 102 LVQPDGVTLEYPNSWNLIANVLYLESFAGVGSYSDDKF-YATNDTEVAQSNFEALQDF 160
QY 187 FOIFPEYKNDFFVVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGAIGDGYSDPESII 246
DB 161 FRUFPPEYKNNKFLVTGYSAGIYIPTLAVLV-----MODPSMNLQGLAVNGLSSEYQND 215
QY 247 GGVAEFLYQIGLDEKQKQYFQKQC-----HECI----- 275
DB 216 NSLVFYFAYHGLGNRLWSSLOTHCCSQNKCNFYDNKDLCEVTNLOEVARIVGNSGLNIY 275
QY 276 -----EHIR-----KQNWFEAFELDKLLDGD-LTSDPS 303
DB 276 -----EHIR-----KQNWFEAFELDKLLDGD-LTSDPS 303
QY 304 YFQNVTCGNSYNNFLRLECTEPEDQLYVVKFSLSPVVRQAIHVGNQTFNDGTIVKEKYLREDT 363
DB 331 -CTNTTAASTYLN-----NPVVRKALNIPBOLPQWDMCNFLVN-----LQYRR--L 373

DB 276 NLYAPCAGGVPSHFYREKDTVVVVDLGNIFTRLPKRMWHQAL-----LRSGDKVRMDPP 330
QY 304 YFQNVTCGNSYNNFLRLECTEPEDQLYVVKFSLSPVVRQAIHVGNQTFNDGTIVKEKYLREDT 363
DB 331 -CTNTTAASTYLN-----NPVVRKALNIPBOLPQWDMCNFLVN-----LQYRR--L 373
QY 364 VQSVKPMLEINNN--YKVLINYGOLDIIVAAALTERSLMGDMW--KSGQETKKAEKKVW 419
DB 374 YRSMNSQYKLKLLSSQKYLILYNGDVMAC-----NFMGDWFVDSLNRQMEVQRREP 426
QY 420 KIFKSDS--EVAGYIRQVGDHFQVILIRGGHLLPYDQPLRAEDMINRFI 466
DB 427 LVKYGDSGEQIAGFVKFESHIAFLTIKGAGHWPVDKPLAFTMFSREL 475

RESULT 11

US-09-702-705-336
/ Sequence 336, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedwick, Tom
/ APPLICANT: Carter, Darrick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 336
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-702-705-336

Query Match 21.8%; Score 557; DB 4; Length 480;
Best Local Similarity 28.0%; Pred. No. 9.2e-50;
Matches 148; Conservative 91; Mismatches 162; Indels 128; Gaps 20;
QY 12 LVLMPGCDGLFHSLSYRSVMPKGDGQPLFLTPYIEAGKIQKRELSLVGPFPL-- 69
DB 1 MIRAAPPFLFLLLLLLLVSWASRGEAAP-----DQDETQR-----LPLAK 43
QY 70 --NMKSAGFLTVNKTNSNLPFWFPFPAIQPEDAPVVLWLOGGPGSSMXGLFVEHGPY 127
DB 44 QPSFRQYSGYL--KSSGSKHLHYWFVESQKDPNSPVVLWNGGPGCSSLDGLLTHGPF 101
QY 128 VV-TSNMTLRDRDPFWTTXSMLYIDNPVGTGFTDTHGYAVNEDDVARLDYLSALIQF 186
DB 102 LVQPDGVTLEYPNSWNLIANVLYLESFAGVGSYSDDKF-YATNDTEVAQSNFEALQDF 160
QY 187 FOIFPEYKNDFFVVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGAIGDGYSDPESII 246
DB 161 FRUFPPEYKNNKFLVTGYSAGIYIPTLAVLV-----MODPSMNLQGLAVNGLSSEYQND 215
QY 247 GGVAEFLYQIGLDEKQKQYFQKQC-----HECI----- 275
DB 216 NSLVFYFAYHGLGNRLWSSLOTHCCSQNKCNFYDNKDLCEVTNLOEVARIVGNSGLNIY 275
QY 276 -----EHIR-----KQNWFEAFELDKLLDGD-LTSDPS 303
DB 276 NLYAPCAGGVPSHFYREKDTVVVVDLGNIFTRLPKRMWHQAL-----LRSGDKVRMDPP 330
QY 304 YFQNVTCGNSYNNFLRLECTEPEDQLYVVKFSLSPVVRQAIHVGNQTFNDGTIVKEKYLREDT 363
DB 331 -CTNTTAASTYLN-----NPVVRKALNIPBOLPQWDMCNFLVN-----LQYRR--L 373

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Qy 364 VQSVKPLWTEIMNN--YKVLIIYNGOLDIIVAAALTEIERSLGMQW--KGSQBYKKAQKQW 419
Db 374 YRSMNSQYLKLLSSQKYQILLYNGDVMAC-----NFMGDEWFVDSLNGQMEVORRPW 426
Qy 420 KIFPKSDS--EVAGYIRQVGDPHOVIIRGGGHILPYDQPLRAFDMINRFI 466
Db 427 LVKYGDSGEOIAGFVKFSHTIAFTIKGAGHWVFTDKFLAAFTWFSRFL 475

RESULT 12
US-09-736-457-336
; Sequence 336: Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 336
; LENGTH: 480
; TYPE: PRt
; ORGANISM: Homo sapiens
US-09-736-457-336

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Qy 420 KIFKSDS--EVAGYIRQVGFHQVILIRGGGHILPYDQPLRAFDMINRRI 466
Db 427 LVKYGDSGEQIAGTFVKFBSFHIAFTLIKAGAHMVPTDKPLAAFTMFSREL 475

RESULT 13
US-09-640-305-4
; Sequence 4, Application US/09640305
; Patent NO. RE37447
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Yeh, Patrice
; TITLE OF INVENTION: MODIFIED KLJYVERONYCES YEASTS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/640,305
; FILING DATE: 16-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,673
; FILING DATE: 06-FEB-1995
; APPLICATION NUMBER: WO PCT/FR93/00623
; FILING DATE: 23-JUN-1993
; APPLICATION NUMBER: FR 92/07785
; FILING DATE: 25-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST92040-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-640-305-4

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Query Match      21.8%; Score 557; DB 4; Length 480;
Best Local Similarity 28.0%; Pred. No. 9.2e-50;
Matches 148; Conservative 91; Mismatches 162; Indels 128; Gaps 20

QY      12 LVLLMPGCDGIFHSLYRSVSNPPKXGDSGQPLFLTPYIEAGKIQKRELSLVGPPQL-- 69
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Db      1 MIRAAPPPLFLLLLLLLLVSWASGEAAP-----DQDEIQR-----LPGLAK 43

QY      70 --NMKSYAGFLTVNKTYSNLSFFWFPPAQIOPEDAPVVLMLQGPGGSKXGLFVHGYP 127
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      44 QSFPROYSGIL--KSGSGKHLHYEVESQKDPENSPVVLMLNGPGGSSLDGLTTHGPPF 101

QY      128 VV-TSNMTLRDRDFPMTTXXSMLYIDNPVGTFGFTDDTHGYAVNEDVDARDLYSALIOF 186
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      102 LVQPDGVTLXNPNYSWNLIANVLYLESFAGVGFYSDDKF-YATNDTEVAQSNFEALQDF 160

QY      187 FOIFPEYKNDPVTYGESVAGKYVPAIAHLIHSNPNRVKINUNGIAIGGYSDPESII 246
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      161 FRLFPEYKNNKLFATGESVAGIYIPTLAFLV-----MDPMSNLOQLAVGNGLSSYEQND 215

QY      247 GGYAEFLYQIGLDEKQKYFKQKC-----HECI----- 275

Db      216 NSLVFYAYTHGLGNRLMSSLQTHCCSQNKCNFYDNKDLCEVTNLQLEVAIRVGNGLNIY 275

QY      276 -----BHIR-----KQNWFEAFELDKLDLGD-LTSDPS 303
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      276 NLYAPCAGVPSPHFYKXDTVVVDLGNIFTRPLKRWHQAL-----LRSGDKVRMDPP 330

QY      304 YFQNVITGCSNYNIFLCTPEPDQLYVYKFLSLPEVQAIIHVGNQTFNDGTVIEKYLREDT 363
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      331 -CTNTTAASTYLN-----NPVVRKALNIPEQLPQWDMCNFLYN-----LQYRR--L 373

QY      364 VQSVKFWLTEIMNN--YKVLINGOLDIIVAAALTEKSLMGDMW--KGSQYKXKAEKVV 419
      ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      374 YRSMNSQYLLSSQKYQIILYNGVDVWAC-----NFMGDEWFDVSLNOKREVORPW 426

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:44:45 ; Search time 36 Seconds
(without alignments)

2270.907 Million cell updates/sec

Title: US-10-084-018-3

Perfect score: 2554

Sequence: 1 MVGAMWKIVSLVLLMPGPC.....RAFDMINRFYKGMDDPYVG 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2550	99.8	476	14	US-10-084-018-3
2	2539	99.4	476	9	US-09-729-674-110
3	2538	99.4	476	10	US-09-909-320-164
4	2538	99.4	476	10	US-09-909-088B-164
5	2538	99.4	476	10	US-09-905-291A-164
6	2538	99.4	476	10	US-09-902-853-164
7	2538	99.4	476	10	US-09-907-824-164
8	2538	99.4	476	10	US-09-907-841-164
9	2538	99.4	476	11	US-09-904-011-164
10	2538	99.4	476	11	US-09-906-742-164
11	2538	99.4	476	11	US-09-906-838-164
12	2538	99.4	476	11	US-09-907-613-164
13	2538	99.4	476	11	US-09-907-942-164
14	2538	99.4	476	11	US-09-796-753-40
15	2538	99.4	476	11	US-09-904-859-164

16	2538	99.4	476	11	US-09-909-204-164	Sequence 164, App
17	2538	99.4	476	11	US-09-904-820-164	Sequence 164, App
18	2538	99.4	476	11	US-09-904-786-164	Sequence 164, App
19	2538	99.4	476	11	US-09-906-646-164	Sequence 164, App
20	2538	99.4	476	11	US-09-906-700-164	Sequence 164, App
21	2538	99.4	476	11	US-09-903-786-164	Sequence 164, App
22	2538	99.4	476	11	US-09-902-903-164	Sequence 164, App
23	2538	99.4	476	11	US-09-903-749A-164	Sequence 164, App
24	2538	99.4	476	11	US-09-904-119-164	Sequence 164, App
25	2538	99.4	476	11	US-09-904-956-164	Sequence 164, App
26	2538	99.4	476	11	US-09-902-736-164	Sequence 164, App
27	2538	99.4	476	11	US-09-907-794-164	Sequence 164, App
28	2538	99.4	476	11	US-09-903-943-164	Sequence 164, App
29	2538	99.4	476	11	US-09-904-462-164	Sequence 164, App
30	2538	99.4	476	11	US-09-907-925-164	Sequence 164, App
31	2538	99.4	476	11	US-09-902-692-164	Sequence 164, App
32	2538	99.4	476	11	US-09-903-520-164	Sequence 164, App
33	2538	99.4	476	11	US-09-905-056-164	Sequence 164, App
34	2538	99.4	476	11	US-09-909-064-164	Sequence 164, App
35	2538	99.4	476	11	US-09-904-553-164	Sequence 164, App
36	2538	99.4	476	11	US-09-905-381-164	Sequence 164, App
37	2538	99.4	476	11	US-09-905-088-164	Sequence 164, App
38	2538	99.4	476	11	US-09-907-575-164	Sequence 164, App
39	2538	99.4	476	11	US-09-905-075-164	Sequence 164, App
40	2538	99.4	476	11	US-09-902-759-164	Sequence 164, App
41	2538	99.4	476	11	US-09-902-634-164	Sequence 164, App
42	2538	99.4	476	11	US-09-902-713-164	Sequence 164, App
43	2538	99.4	476	11	US-09-907-979-164	Sequence 164, App
44	2538	99.4	476	11	US-09-902-615-164	Sequence 164, App
45	2538	99.4	476	11	US-09-903-925-164	Sequence 164, App

ALIGNMENTS

RESULT 1

US-10-084-018-3
; Sequence 3, Application US/10084018
; Publication NO. US20020160499A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hawkins, Phillip R.
; Hillman, Jennifer L.
; Lal, Preeti
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,018
; FILING DATE: 25-Feb-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,689A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/828,488
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:

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, , TELEPHONE: 415-855-0555
, , -
, , TELEFAX: 415-845-4166
, , INFORMATION FOR SEQ ID NO: 3:
, ,
, , SEQUENCE CHARACTERISTICS:
, ,
, , LENGTH: 476 amino acids
, , TYPE: amino acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
, , IMMEDIATE SOURCE:
, , LIBRARY: MMLR3DT01
, , CLONE: 566993
, , SEQUENCE DESCRIPTION: SEQ ID
US-10-084-018-3

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Query Match	99.8%; Score 2550; DB 14; Length 476;
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DB	
QY	1 MVGAMKVTISLVLLMPCGDCGLFHSLYRSVSMPPKGDSCQPLFLTPYIEAGKIQKREL 60
DB	
QY	61 SLVGPPPLGNMKSAGFTVTKNTNSNLFWFPFPAIQPEDAPVVLWOGGPGGSSMKGL 120
DB	
QY	61 SLVGPPPLGNMKSAGFTVTKNTNSNLFWFPFPAIQPEDAPVVLWOGGPGGSSMKGL 120
DB	
QY	121 FVEHGPVYVTSNMTLRDRDFPWTXXSMLYIDNPVGGFSFTDDTHGYAVNEDDVARLDY 180
DB	
QY	121 FVEHGPVYVTSNMTLRDRDFPWTXXSMLYIDNPVGGFSFTDDTHGYAVNEDDVARLDY 180
DB	
QY	181 SALIQFOIFPEYKNDPVYVTGESYAGKYVPAIAHLIHSLNPREVKINLNGIAIGDGY 240
DB	
QY	181 SALIQFOIFPEYKNDPVYVTGESYAGKYVPAIAHLIHSLNPREVKINLNGIAIGDGY 240
DB	
QY	241 DPESIIGGVAEFLYQIGLLDBKQKYFKQKQCEHIEHIRKQNFPEAFETLKLDDGLTS 300
DB	
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DB	
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QY	301 DPSYFQNVTCGSNNYFNLCTPEPDQLYYVKFSLPEVROALIHVGNOTFNDGTIVEKYLR 360
DB	
QY	361 EDTVOSVXPWLTEINNNYKVLINYQLDIIVAALATERSLGMWMDKGSOEYKKAEEKYWK 420
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QY	361 EDTVOSVXPWLTEINNNYKVLINYQLDIIVAALATERSLGMWMDKGSOEYKKAEEKYWK 420
DB	
QY	421 IFKSDSEVAGYIRQVGDPHQVIIRGGGHILPYDQPLFAFDMINRFTYXKGWDPYVG 476
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RESULT 2
US-09-729-674-110
; Sequence 110, Application US/09729674
; Patent No. US2001003935A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Collins-Rache, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steiningger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Echtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEIN
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/772

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; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 476
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-729-674-110

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Query Match	99.4%;	Score 2539;	DB 9;	Length 476;																		
Best Local Similarity	99.2%;	Pred. No. 2.3e-237;																				
Matches 472;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;																		
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Db	1	MVGAMKVI	VS	LVLLMPG	CDGLF	HSLSY	SVS	MPK	GD	SCQ	PLF	FL	TPY	I	EAG	KI	Q	K	R	E	L	60
Qy	61	SLVGP	PPGL	NM	K	S	Y	A	G	E	L	T	V	N	K	T	Y	N	S	N	L	120
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Qy	121	FVESHG	P	V	V	T	S	N	M	L	R	D	R	P	P	M	T	T	S	M	L	180
Db	121	FVESHG	P	V	V	T	S	N	M	L	R	D	R	P	P	M	T	T	S	M	L	180
Qy	181	SALIQ	F	Q	F	I	P	P	E	Y	K	N	D	F	V	Y	T	G	S	Y	A	240
Db	181	SALIQ	F	Q	F	I	P	P	E	Y	K	N	D	F	V	Y	T	G	S	Y	A	240
Qy	241	DPESI	I	G	G	V	A	E	F	I	Y	Q	L	L	D	E	K	O	K	Y	F	300
Db	241	DPESI	I	G	G	V	A	E	F	I	Y	Q	L	L	D	E	K	O	K	Y	F	300
Qy	301	DP	S	F	Q	N	V	T	G	S	N	Y	N	F	L	R	C	T	E	P	D	360
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Qy	361	EDT	V	S	V	K	P	L	T	E	I	M	N	N	Y	K	V	I	I	N	G	420
Db	361	EDT	V	S	V	K	P	L	T	E	I	M	N	N	Y	K	V	I	I	N	G	420
Qy	421	I	F	K	S	D	E	V	A	G	I	R	Q	V	G	D	F	H	Q	V	I	476
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RESULT 3
US-09-309-320-164
; Sequence 164, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Garritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 164
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-909-088B-164

Query Match 99.4%; Score 2538; DB 10; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60

Qy 61 SLVGPPFGLNKSAGFLTVNKTNSNLPFWFFPAIQPEDAPVVLMLQGGPGSSMXGL 120
Db 61 SLVGPPFGLNKSAGFLTVNKTNSNLPFWFFPAIQPEDAPVVLMLQGGPGSSMXGL 120

Qy 121 FVEHGPVVTNSMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNSMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180

Qy 181 SALIQFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKNLNGIAIGDYS 240
Db 181 SALIQFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKNLNGIAIGDYS 240

Qy 241 DPESIIIGYAEFLVQIGLLDSEKQKXFKQKQHECHIEHIRKQWFEAFIELDKLDGLTS 300
Db 241 DPESIIIGYAEFLVQIGLLDSEKQKXFKQKQHECHIEHIRKQWFEAFIELDKLDGLTS 300

Qy 301 DPSYFQNVTCGNSYNFRLCTEPEDOLYYVKSLSPEVROAIHVGNOTFNDGTIVEKYL 360
Db 301 DPSYFQNVTCGNSYNFRLCTEPEDOLYYVKSLSPEVROAIHVGNOTFNDGTIVEKYL 360

Qy 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIVAALTERSLMGMDWKSGQYKKAEEKVWK 420
Db 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIVAALTERSLMGMDWKSGQYKKAEEKVWK 420

Qy 421 IFKSDSEVAGYIRQAGDFHVIIRGGGHILPYDQPLRAFDMINRFIYKGDHPYVG 476
Db 421 IFKSDSEVAGYIRQAGDFHVIIRGGGHILPYDQPLRAFDMINRFIYKGDHPYVG 476

RESULT 5
US-09-905-291A-164
; Sequence 164, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 164
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-905-291A-164

Query Match 99.4%; Score 2538; DB 10; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60

Qy 61 SLVGPPFGLNKSAGFLTVNKTNSNLPFWFFPAIQPEDAPVVLMLQGGPGSSMXGL 120
Db 61 SLVGPPFGLNKSAGFLTVNKTNSNLPFWFFPAIQPEDAPVVLMLQGGPGSSMXGL 120

Qy 121 FVEHGPVVTNSMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNSMTLRDRDPFWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180


```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 164
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-824-164

Query Match          99.4%; Score 2538; DB 10; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

; QY 1 MVGAMKVIIVSLVLLMPGCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKREL 60
; |||||
; 61 SLVGPFPGLNPKSYAGFLTVNKTYSNLFNFWFFPAIQPEDAPVVLWLOGPGGSSNKKGL 120
; |||||
; 61 SLVGPFPGLNPKSYAGFLTVNKTYSNLFNFWFFPAIQPEDAPVVLWLOGPGGSSNFKGL 120
; |||||
; 121 FVEHGPVVTNSMTLRDRDPFWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
; |||||
; 121 FVEHGPVVTNSMTLRDRDPFWTTTUSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
; |||||
; 181 SALIQFFQIFPEYKNNDFVVTGESYAGKVPAIAHLIHSNLPVREVKINLNGIAIGDGY 240
; |||||
; 181 SALIQFFQIFPEYKNNDFVVTGESYAGKVPAIAHLIHSNLPVREVKINLNGIAIGDGY 240
; |||||
; 241 DPESIIGGYAEFLYQIGLLDEKQKQYFQKQCHIEHIRKQNWFEAFELDKLLDGLTS 300
; |||||
; 241 DPESIIGGYAEFLYQIGLLDEKQKQYFQKQCHIEHIRKQNWFEAFELDKLLDGLTS 300
; |||||
; 301 DPYFQNVGTGCSNYYNFLRCTEPEDQLYVVKFLSLPEVROAIVHGNQTFNDGTIVEKYL 360
; |||||
; 301 DPYFQNVGTGCSNYYNFLRCTEPEDQLYVVKFLSLPEVROAIVHGNQTFNDGTIVEKYL 360
; |||||
; 361 EDTVQSVKPLTEIMNMYKVLINYGOLDIIVAAALTEFLSLMGMDKSGQYKKAEEKVWK 420
; |||||
; 361 EDTVQSVKPLTEIMNMYKVLINYGOLDIIVAAALTEFLSLMGMDKSGQYKKAEEKVWK 420
; |||||
; 421 IPKSDSEVAGYIRQAGDFHQVIRGGGHILPYDQPLRAFDMINRFTYKGMWDPYVG 476
; |||||
; 421 IPKSDSEVAGYIRQAGDFHQVIRGGGHILPYDQPLRAFDMINRFTYKGMWDPYVG 476
; |||||

RESULT 8
US-09-907-841-164
; Sequence 164, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Timothy A.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

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;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 164
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-907-841-164

Query Match 99.4%; Score 2538; DB 10; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60

QY 61 SLVGPPFGLNMKSYAGFLTNKNTYNSNLFVFWFFPAQIQPEDAPVVLWLOGGPGGSSMXGL 120
Db 61 SLVGPPFGLNMKSYAGFLTNKNTYNSNLFVFWFFPAQIQPEDAPVVLWLOGGPGGSSMXGL 120

QY 121 FVEHGPVVTNSMTLRDRDPWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNSMTLRDRDPWTTTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180

QY 181 SALIQFQIFPEYKNNDFYVTGESYAGKYVPAIAHLHLSNPVREVKNINLNGIAIGDGY 240
Db 181 SALIQFQIFPEYKNNDFYVTGESYAGKYVPAIAHLHLSNPVREVKNINLNGIAIGDGY 240

QY 241 DPESIIGGYAEFLYQIGLLEKOKKYFQKOCHECHIRKONWFEAFIILDKLLDGLTS 300
Db 241 DPESIIGGYAEFLYQIGLLEKOKKYFQKOCHECHIRKONWFEAFIILDKLLDGLTS 300

QY 301 DPYFQNVTCGSNYNFLRCTEPEDDQLYYVKFLSLPEVROAIHVGNOTFNDGTIVEKYL 360
Db 301 DPYFQNVTCGSNYNFLRCTEPEDDQLYYVKFLSLPEVROAIHVGNOTFNDGTIVEKYL 360

QY 361 EDTVQSVKPLTEIMNNKYVLIYNGQLDIIIVAAALTELSLGMGMKGSQYKKAEEKVWK 420
Db 361 EDTVQSVKPLTEIMNNKYVLIYNGQLDIIIVAAALTELSLGMGMKGSQYKKAEEKVWK 420

QY 421 IFKSDSEVAGYIRQVGFHVIIRGGHILPYOQPLRAFDMINRFYKGGWDPIYVG 476
Db 421 IFKSDSEVAGYIRQVGFHVIIRGGHILPYOQPLRAFDMINRFYKGGWDPIYVG 476

RESULT 9

US-09-904-011-164
; Sequence 164, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

Query Match 99.4%; Score 2538; DB 11; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMWKVIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60

QY 61 SLVGPPFGLNMKSYAGFLTNKNTYNSNLFVFWFFPAQIQPEDAPVVLWLOGGPGGSSMXGL 120

Db 61 SLVGGPFGLNKMSYAGFLTVNKTNSNLFVFWFFPAQIQPEDAPVVLWLGPGGSSMFGL 120
Qy 121 FVEHGPVVTNSMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNSMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
Qy 181 SALIOFFQIIFPEYKNDPVYVTSYAGKYVPATAHLHSLNPVREVKNLNGTAIGDYS 240
Db 181 SALIOFFQIIFPEYKNDPVYVTSYAGKYVPATAHLHSLNPVREVKNLNGTAIGDYS 240
Qy 241 DPESIIGGYAEFLYQIGLLDEKQKYYFQKQCEHIEHIRKQNWFEAFIILDKLDDGLTS 300
Db 241 DPESIIGGYAEFLYQIGLLDEKQKYYFQKQCEHIEHIRKQNWFEAFIILDKLDDGLTS 300
Qy 301 DPSYFQNTGCSNYYNFRCTEPEDQLYYVKFSLPEVROAIHVGNQTFNDGTIVKYL 360
Db 301 DPSYFQNTGCSNYYNFRCTEPEDQLYYVKFSLPEVROAIHVGNQTFNDGTIVKYL 360
Qy 361 EDTVQSVKPNLWTEIMNNYKVLINYGQDIIIVAAALTSRLMGMDWKGSGQYKKAQKVK 420
Db 361 EDTVQSVKPNLWTEIMNNYKVLINYGQDIIIVAAALTSRLMGMDWKGSGQYKKAQKVK 420
Qy 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476
Db 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

RESULT 10

US-09-906-742-164
; Sequence 164, Application US/09906742
; Publication No. US20030023054A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 164
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-164

Query Match 99.4%; Score 2538; DB 11; Length 476;

Best Local Similarity 99.2%; Pred. No. 2.8e-237;

Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MVGNMKVTVSLVLLMPCDGLPHSLYRSVSMPPKSGDPLFTPTVTEAGKIOKREL 60
Db 1 MVGNMKVTVSLVLLMPCDGLFRSLYRSVSMPPKSGDPLFTPTVTEAGKIOKREL 60
Qy 61 SLVGGPFGLNKMSYAGFLTVNKTNSNLFVFWFFPAQIQPEDAPVVLWLGPGGSSMFGL 120
Db 61 SLVGGPFGLNKMSYAGFLTVNKTNSNLFVFWFFPAQIQPEDAPVVLWLGPGGSSMFGL 120
Qy 121 FVEHGPVVTNSMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNSMTLRDRDPFWTTXSMLYIDNPVGTGFSFTDTHGYAVNEDDVARDLY 180
Qy 181 SALIOFFQIIFPEYKNDPVYVTSYAGKYVPATAHLHSLNPVREVKNLNGTAIGDYS 240
Db 181 SALIOFFQIIFPEYKNDPVYVTSYAGKYVPATAHLHSLNPVREVKNLNGTAIGDYS 240
Qy 241 DPESIIGGYAEFLYQIGLLDEKQKYYFQKQCEHIEHIRKQNWFEAFIILDKLDDGLTS 300
Db 241 DPESIIGGYAEFLYQIGLLDEKQKYYFQKQCEHIEHIRKQNWFEAFIILDKLDDGLTS 300
Qy 301 DPSYFQNTGCSNYYNFRCTEPEDQLYYVKFSLPEVROAIHVGNQTFNDGTIVKYL 360
Db 301 DPSYFQNTGCSNYYNFRCTEPEDQLYYVKFSLPEVROAIHVGNQTFNDGTIVKYL 360
Qy 361 EDTVQSVKPNLWTEIMNNYKVLINYGQDIIIVAAALTSRLMGMDWKGSGQYKKAQKVK 420
Db 361 EDTVQSVKPNLWTEIMNNYKVLINYGQDIIIVAAALTSRLMGMDWKGSGQYKKAQKVK 420
Qy 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476
Db 421 IFKSDSEVAGYIRQAGDFHQVIRGGHILPYDQPLRAFDMINRFYKGMWDPYVG 476

RESULT 11

US-09-906-838-164
; Sequence 164, Application US/09906838
; Publication No. US20030027143A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIORITY APPLICATION NUMBER: 09/665,350
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 164
LENGTH: 476
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-164

Query Match 99.4%; Score 2538; DB 11; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MYGAMKUIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIOKREL 60
DB 1 MYGAMKUIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIOKREL 60
QY 61 SLVGPPFGLNMKSYAGFLTVNKTYNSNLFVFWFFPAQIQPEDAPVVLWQGGPGSSMKGL 120
DB 61 SLVGPPFGLNMKSYAGFLTVNKTYNSNLFVFWFFPAQIQPEDAPVVLWQGGPGSSMKGL 120
QY 121 FVEHGPYVVTSMNLTDRDPFWTTTYSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDIY 180
DB 121 FVEHGPYVVTSMNLTDRDPFWTTTYSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDIY 180
QY 181 SALIQFQIFPEYKNDYVVTGESYAGKYVPAIAHLIHSLNPRVVKINLNGAIGDGYVS 240
DB 181 SALIQFQIFPEYKNDYVVTGESYAGKYVPAIAHLIHSLNPRVVKINLNGAIGDGYVS 240
QY 241 DPESIIGGYAEFLYQIGLLDEKQKXFKQCHCEHIEHIRKQNWFEAFELDKLDDGLTS 300
DB 241 DPESIIGGYAEFLYQIGLLDEKQKXFKQCHCEHIEHIRKQNWFEAFELDKLDDGLTS 300
QY 301 DPSYFQNTVGTCSNYYNFLRCTEPEDQLYVVKFSLPEVRQAIVHGNQTFNDGTIVEKYLR 360
DB 301 DPSYFQNTVGTCSNYYNFLRCTEPEDQLYVVKFSLPEVRQAIVHGNQTFNDGTIVEKYLR 360
QY 361 EDTQSVKPKWLTETIMNNYKVLTYNGOLDIIVAAALTESLGMGMKSGOEYKKAKKVWK 420
DB 361 EDTQSVKPKWLTETIMNNYKVLTYNGOLDIIVAAALTESLGMGMKSGOEYKKAKKVWK 420
QY 421 IFKSDSEVAGYIRQVGFHQVIRGGGHILPYDQPLRAFDMINRFRYKGMDDPYVG 476
DB 421 IFKSDSEVAGYIRQVGFHQVIRGGGHILPYDQPLRAFDMINRFRYKGMDDPYVG 476

RESULT 12
US-09-907-613-164
Sequence 164, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17


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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 164
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-942-164

Query Match          99.4%; Score 2538; DB 11; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
QY 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGPGGSSMFL 120
Db 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGPGGSSMFL 120
QY 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIOFFQIIPPEYKXNDFFVTGSEYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDYS 240
Db 181 SALIOFFQIIPPEYKXNDFFVTGSEYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDYS 240
QY 241 DPESIIGGVAEFLYQIGLDEKOKKYFQKQCHIEHIRKQNFPEAFELDKLLDGLDLS 300
Db 241 DPESIIGGVAEFLYQIGLDEKOKKYFQKQCHIEHIRKQNFPEAFELDKLLDGLDLS 300
QY 301 DPSYFQNVTCGSNNYINFLRTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYL 360
Db 301 DPSYFQNVTCGSNNYINFLRTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYL 360
QY 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIIVAAALTEFLMGMWDMKGSQYKAEKKVWK 420
Db 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIIVAAALTEFLMGMWDMKGSQYKAEKKVWK 420
QY 421 IFKSDSEVAGYIRQAGDFHVIIRGGGHILPYDOPARAFDMINRFYKGMWDYPVG 476
Db 421 IFKSDSEVAGYIRQAGDFHVIIRGGGHILPYDOPARAFDMINRFYKGMWDYPVG 476

RESULT 14
US-09-796-753-40
; Sequence 40, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 40
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-753-40

Query Match          99.4%; Score 2538; DB 11; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
Db 1 MVGAMKVIIVSLVLLMPGCDGLFHSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKREL 60
QY 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGPGGSSMFL 120
Db 61 SLVGPPFGLNPKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLOGPGGSSMFL 120
QY 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPVVTNNLTDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
QY 181 SALIOFFQIIPPEYKXNDFFVTGSEYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDYS 240
Db 181 SALIOFFQIIPPEYKXNDFFVTGSEYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDYS 240
QY 241 DPESIIGGVAEFLYQIGLDEKOKKYFQKQCHIEHIRKQNFPEAFELDKLLDGLDLS 300
Db 241 DPESIIGGVAEFLYQIGLDEKOKKYFQKQCHIEHIRKQNFPEAFELDKLLDGLDLS 300
QY 301 DPSYFQNVTCGSNNYINFLRTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYL 360
Db 301 DPSYFQNVTCGSNNYINFLRTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYL 360
QY 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIIVAAALTEFLMGMWDMKGSQYKAEKKVWK 420
Db 361 EDTVQSVKPLTEIMNNYKVLINQGLDIIIVAAALTEFLMGMWDMKGSQYKAEKKVWK 420
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QY 421 IFKSDSEVAGYIRQVGHQVHVIIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476
Db 421 IFKSDSEVAGYIRQVGHQVHVIIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476

RESULT 15

US-09-904-859-164
; Sequence 164, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 164
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-164

Query Match 99.4%; Score 2538; DB 11; Length 476;
Best Local Similarity 99.2%; Pred. No. 2.8e-237;
Matches 472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVGANMKIVISLVLLMPGCDGLFHSLYRSVSMPPKSGDGLFLFTPIEAGKIQKREL 60
Db 1 MVGANMKIVISLVLLMPGCDGLFHSLYRSVSMPPKSGDGLFLFTPIEAGKIQKREL 60

QY 61 SLVGPPPGLNKMSYAGELTVNKTYSNLFVFFFPQAIQPEDAPVVLWLGSGGSMKGL 120
Db 61 SLVGPPPGLNKMSYAGELTVNKTYSNLFVFFFPQAIQPEDAPVVLWLGSGGSMFGL 120

QY 121 FVEHGPYVVTSMNLTDRDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180
Db 121 FVEHGPYVVTSMNLTDRDRDPWTTTXXSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY 180

QY 181 SALIOFFQIFPEYKNDYFVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGY 240
Db 181 SALIOFFQIFPEYKNDYFVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGY 240

QY 241 DPESIIIGGYAEFLYQIGLLDEKOKKYFOKOCHECHIRKQNWPEAFELDKLLDGLTS 300
Db 241 DPESIIIGGYAEFLYQIGLLDEKOKKYFOKOCHECHIRKQNWPEAFELDKLLDGLTS 300

QY 301 DPSYFQNVGTGCSNYNFLRCTEPEPOLYVYKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR 360
Db 301 DPSYFQNVGTGCSNYNFLRCTEPEPOLYVYKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR 360

QY 361 EDTVQSVKFWLTEIMNNYKVLINYGOLDIIVAAALTEKSLMGMDKSGOEYKKAQKWK 420
Db 361 EDTVQSVKFWLTEIMNNYKVLINYGOLDIIVAAALTEKSLMGMDKSGOEYKKAQKWK 420

QY 421 IFKSDSEVAGYIRQVGHQVHVIIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476
Db 421 IFKSDSEVAGYIRQVGHQVHVIIRGGHILPYDQPLRAFDMINRFYKGGWDPYVG 476

Search completed: November 7, 2003, 16:50:23
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:41:14 ; Search time 21 Seconds
(without alignments)
2179,823 Million cell updates/sec

Title: US-10-084-018-3
Perfect score: 2554
Sequence: 1 MVGAMKVIIVSLVLLMPGPC.....RAFDMINRFYKGGNDPYVG 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	894.5	35.0	441	2 A41612	vitellogenic carbo
2	623.5	24.4	444	2 D86283	tl5d22.4 protein -
3	585.5	22.9	500	1 S22330	carboxypeptidase C
4	571.5	22.4	510	2 T48977	carboxypeptidase-1
5	567.5	22.2	411	1 A35375	carboxypeptidase C
6	557	21.8	480	2 A31589	carboxypeptidase C
7	556	21.8	429	1 T03607	probable carboxype
8	555.5	21.8	499	1 A29412	carboxypeptidase C
9	536	21.0	474	2 A35732	protective protein
10	503	19.7	2105	2 T18968	probable serine-ty
11	491	19.2	454	2 T20829	probable serine ca
12	484	19.0	482	2 T49079	serine-type carbox
13	483.5	18.9	542	1 J31380	carboxypeptidase C
14	481.5	18.9	516	2 S44191	carboxypeptidase D
15	479.5	18.8	469	2 T16316	probable serine ca
16	471	18.4	508	1 S46008	probable carboxype
17	466.5	18.3	456	2 A85139	hypothetical prote
18	466.5	18.3	501	2 T49081	serine-type carbox
19	465.5	18.2	552	2 J37666	serine-type carbox
20	463.5	18.1	2338	2 T25810	hypothetical prote
21	460	18.0	502	2 T49188	serin carboxypepti
22	455	17.8	1002	2 T43236	carboxypeptidase C
23	454	17.8	479	2 G96501	probable serine ca
24	451	17.7	465	2 G86244	Serine carboxypept
25	447.5	17.5	499	1 CPB8S	carboxypeptidase C
26	446	17.5	482	2 A43828	probable serine ca
27	442.5	17.3	523	1 S61713	carboxypeptidase C
28	434.5	17.0	456	2 H86406	probable serine ca
29	432.5	16.9	510	1 S43516	carboxypeptidase C

30 432 16.9 425 2 E84631 probable serine ca
31 432 16.9 532 1 CPBYV carboxypeptidase C
32 431.5 16.9 458 2 F84746 probable serine ca
33 429 16.8 452 2 H84772 probable serine ca
34 428.5 16.8 423 1 A29639 carboxypeptidase D
35 426 16.7 487 2 T49080 serine-type carbox
36 422.5 16.5 447 2 G84772 probable serine ca
37 422.5 16.5 487 2 B84472 probable serine ca
38 421 16.5 480 2 T50511 serine-type carbox
39 419.5 16.4 510 2 T39601 serine carboxypept
40 417.5 16.3 425 2 F85360 SERINE CARBOXYPEPT
41 417 16.3 468 2 D84503 probable serine ca
42 416 16.3 470 2 B96637 hypothetical prote
43 415 16.2 465 2 B85358 SERINE CARBOXYPEPT
44 410 16.1 512 2 T33463 probable serine ca
45 410 16.1 574 2 T16230 hypothetical prote

vitellogenic carboxypeptidase (EC 3.4.16.-) precursor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 17-Mar-2000
C:Accession: A41612
R:Cho, W.L.; Deitsch, K.W.; Raikhel, A.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 10821-10824, 1991
A:Title: An extraovarian protein accumulated in mosquito oocytes is a carboxypeptidase
A:Reference number: A41612; MUID:92073379; PMID:1961751
A:Accession: A41612
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-441 <CHO>
A:Cross-references: GB:MT9452; NID:gl59555; PID:g473361
C:Superfamily: serine carboxypeptidase
C:Keywords: hydrolase; serine carboxypeptidase

Query Match 35.0%; Score 894.5; DB 2; Length 441;
Best Local Similarity 43.4%; Pred. No. 3.5e-59;
Matches 175; Conservative 87; Mismatches 132; Indels 9; Gaps 6;

QY 24 FHSLYRSVSMPPK-GDSQQPLFLPTPIEAGKIQKRELSLVGPPFGLMKSVAGELTVNK 82
DB 26 YKKLMRGSGASPRRGESGEPLFLTELLQDGKIEEARNKARVNHNPMLSSVESYSGMTYDA 85
QY 83 TVNSNLPFWFPFAQIQEDAPVVLWLGPGGSSMXGLFVEHGPYVTSNMTLRDRDFPW 142
DB 86 KHNSNLFYVYPAKNRQAPILVWLGPGGASSLFGMFEENGPFPHIHRNNSVKQREYSW 145
QY 143 TTTXSMLYIDNPVGTFGRFTDDTHGYAVNEDDVARDLYSALIQFOIFPEYKQNDYFTVG 202
DB 146 HONHMIYIDNPVGTFGRFTDSDEGYSTNEEHVGENLMKFIQQFVLFPNLKHFYISG 205
QY 203 ESYAGKYVPAHLHLSNPVREKINLNGAIGDYSDDPESIIGGYAEFLYQIGLLDEK 262
DB 206 ESYGKFPVAFGYAH--NSQSPKINLQGLAIGDGYDPLNQL-NYGEYLYELGLIDLN 262
QY 263 QKKYFQKQCHEICIEHRKNWFPEIIDLKDLGDLTSDPSYFQNTGSGNTYNEFURCTE 322
DB 263 GRKKFDEDTAAALACAEKMKCNRLIQLGLFDG-LDQESYFKKVTGPFSSYNYFKGDE 321
QY 323 PDDQ-LYYVKLSLEPVRQATHVGNQTFENDG---TIVEKYREDYVQSKPMLTMINNY 378
DB 322 ESKQSDVLMFELNSNPENVRKHVHGLPFPDSDGNKNKVAEMLSEDTLDTVAPWVSKLSHY 381
QY 379 KVLVYNGOLDIIVAAALTERSLMGMDWKGSOYKKAEEKKWKI 421
DB 382 RVLVYNGQLDIICAYPMTVDLTKMPFDPDSEYKCANREIYRV 424

RESULT 2

D86283
T15D22.4 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: D86283
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86283
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <STO>
A:Cross-references: GB:AE005172; NID:G6899645; PIDN:AAF31022.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match	24.4%;	Score 623.5;	DB 2;	Length 444;
Best Local Similarity	35.2%;	Pred. No. 6.7e-39;		
Matches 145;	Conservative 74;	Mismatches 172;	Indels 21;	Gaps 9
Qy	66	PPGLNMKSYAGFLTVNKTYNSLNLFPPFAQIQP----	EDAPVVLWLOGGGGSSMXGLF	121
Db	28	PPDEALPTKSGVLPVKPAPGSGSMFAFTEAQ-EPTT	PLDPLVLWLOGGGCCSMIGNF	86
Qy	122	VEHGPFVYVTSNMTLRDRD-FPWMTTXXSLYIDNP	VGTFGSFTDDTHGYAVNEDDVARDLY	180
Db	87	YELGFWRVVSRATDLERNPGAWNRFLGLFVDNP	IGVGFSIAASQQDIPTRQORVAEHL	146
Qy	181	SALTQFPFOIFREYKNDNFVVTGESYAGKYVPAIA	HLIHSLPVREKINLNGIALGDGVS	240
Db	147	AALVEFLQNSFENRPFYFTGESYAGKYVPAIGYII	LKEKP--NGKYNLKGAIINGLIT	204
Qy	241	DPESTIGGYABFLYQIGLLDEKQKKYFKQCHECI	EHIRKQNWFEAFETDKLLDGDGLTS	300
Db	205	DPVTQVQTHAVNVVYSGLVNAKQRVELQKAQEI	SVALVKSQKWEAADARTELL-----	258
Qy	301	DPSIFQNTGCSNYNFIPLCTEPEDQLYVVKFLS	LPFVRQAIHVGNQT-FND-GTIVKY	358
Db	259	--TLLSNMTGLATLNTARAIPYRTDL-VVDLLN	QREAKRVLGVSFETVRFEECSDEVEDV	315
Qy	359	LREDTVQSVKFWLTIEMNMYKVLIINGOLDITVA	AAALTELSLIMGDMWKSQBYKAEKKV	418
Db	316	LRADVMKSVKFWVEALSETQVLLYQGMLLDRD	GVVSTEEWMKTNWNSGLGNFSTARRV	375
Qy	419	WKIFKSDSEVAGYIRQVGDHFQVITIRGGGHILP	YQOPLRAFPMINRFYVGK	470
Db	376	WK--DEDGVAGYVQRWGNLCHVATGTAGHFVPTD	KAVNSRDMIEGWLK	425

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RESULT 3
S22530
carboxypeptidase C (EC 3.4.16.5) precursor - rice
N/Alternate names: carboxypeptidase III
C/Species: Oryza sativa (rice)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Nov-1999
C/Accession: S22530
R/Washio, K.; Ishikawa, K.
Plant Mol. Biol. 19, 631-640, 1992
A/Title: Structure and expression during the germination of rice seeds of t
A/Reference number: S22530; MUID:92329723; PMID:162776
A/Accession: S22530
A/Molecule type: DNA
A/Residues: 1-500 <WAS>
A/Cross-references: EMBL:S40458
C/Genetics:

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A: Introns: 100/2; 156/3; 196/3; 244/3; 295/1; 324/3; 411/1; 455/3
C: Superfamily: serine carboxypeptidase
C: Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen
F: 1-21/Domain: signal sequence #status predicted <SIG>
F: 22-73/Domain: propeptide #status predicted <PRO>
F: 74-484/Product: carboxypeptidase C #status predicted <MAT>
F: 485-499/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
F: 144/Binding site: carboxylate (Asn) (covalent) #status predicted
F: 216,404,461/Active site: Ser, Asp, His #status predicted

Query Match 22.9%; Score 585.5; DB 1; Length 500;
Best Local Similarity 29.6%; Pred. No. 5.6e-36;
Matches 149; Conservative 103; Mismatches 195; Indels 57; Gaps 15

Qy 1 MVGAMKVIYSLVLLMPQC-DGL-----FSLYRSVSMPPK-----GSGS 40
Db 1 MATARVSLILLVVLAASACAEGRLPRDAKFPAAQAERLIRSNLLPKEAGPTCAGD-- 58

Qy 41 QPLFLTPYIENAGTKQKRELSLVGPPGL-NMKSYAGELTNKYNLSNLFWFPPAQIQP 99
Db 59 ----VPSVAPGELLE-RVTLPLGPGQVGLGHHAGYIRLPNTHDARMFYLFESRGKK 112

Qy 100 EDAPVWLWLGPGGSSMXGLFVHGPRVVVTSNMTLRDRDPWTTTXXSMLYIDNPVGTGF 159
Db 113 ED-PVILWLTGPGCSSELAIFYENGPFITISNNMSLAWNKGWDITISNIIPVDQPTGTGF 171

Qy 160 SFTDDTHGYAVNEDDVARLDYLSALIQFQIFPEFYKNNDFVVTGESYAGKYPAIAHLIHS 219
Db 172 SYSSDDRDTRHDETVGSDNLYSFLQVFKHPPEAKNDFITGESYAGHYIPAFASRVHQ 231

Qy 220 LNFVRE-VKINLNGIAGDGYSDPESIGGYAEFLYQIGLDEKOKKYFQKCHCEIHI 278
Db 232 GNKANEGIHNLKGLFAINGLTDPAIQYKATDYALDMNLKKSDYDRINKFIPCEPAI 291

Qy 279 R-----KQWFEAFELDKLLDGLTSDPSYFQVNTGCSNXYNPLRTEPEDQLY--- 329
Db 292 KLCOTNGKASCAAAIYWCNSIF-----SSIKVLGTRKNYIDVRK--EEGKLCUDPS 341

Qy 330 --VKFLSLPEVQRAIHVGNQTF-NDGTIVKEYLRREDTVQSVKPLMTEIM-NNYKVIYNG 385
Db 342 NLEKFFGDKA VKEAIGVGDLEFVSCSTTVYQAMLTDMRNLEVGIPALLEDGINVLVIAG 401

Qy 386 QLDIIVAAALTEKSLGMDWKGSQBYKAEKKWKI PKSDSEVAGYIRQVGFHOVIIRG 445
Db 402 EYDLICNWLGNRSRVHSMENSGQKDFVSSHESP---FVVDGAEAGVLKSHGSPSLFKVHN 458

Qy 446 GCHTLPYDQPLRAFDMINRRTYIK 469
Db 459 AGHVMFMDPKASLEMLRRFTQK 482

RESULT 4
T48977
carboxypeptidase-like protein F14D17.80 [imported] - Arabidopsis thaliana
C: Species: Arabidopsis thaliana (mouse-ear cress)
C: Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 24-Oct-2000
R: Jordan, N.; Bangerter, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; I
C: Accession: T48977
A: Reference number: 225008

RESULT 4
T48977

carboxypeptidase-like protein F14D17.80 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 24-Oct-2000
C/Accession: T48977
R/Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Mewes, H.W.
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z25008
A/Accession: T48977
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-510 <JOR>
A/Cross-references: EMBL:AL353992; GSPDB:GN00061; ATSP:F14D17.80
A/Experimental source: cultivar Columbia; BAC clone F14D17
A/Genetics:
A/Gene: NTSP:F14D17.80
A/Map position: 3
A/Introns: 115/2; 171/3; 211/3; 259/3; 310/1; 341/3; 428/1; 472/3
C/Superfamily: serine carboxypeptidase
F/321.421.478/Active site: Ser, Asp, His #status predicted

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:38:00 ; Search time 18 Seconds
(without alignments)
1243.595 Million cell updates/sec

Title: US-10-084-018-3

Perfect score: 2554

Sequence: 1 MVGAMWKIVSLVLMGPGC.....RAFDMINRFYCKGWDPYVG 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2527	98.9	476	1 CPVL HUMAN	Q9h3g5 homo sapien
2	1014	39.7	471	1 VCP AEDAE	P42860 aedes aegypt
3	585.5	22.9	500	1 CBP3 ORISA	P37891 oryza sativ
4	576	22.6	508	1 CBP3 HORVU	P21529 hordeum vul
5	566.5	22.2	516	1 CBP3 ARATH	P32826 arabidopsis
6	556	21.8	429	1 CBP3 ORISA	P52712 oryza sativ
7	555.5	21.8	500	1 CBP3 WHEAT	P11515 triticum ae
8	555	21.7	480	1 PRTP HUMAN	P10619 homo sapien
9	536	21.0	474	1 PRTP MOUSE	P16675 mus musculus
10	491	19.2	454	1 YUA6 CAEL	P52715 caenorhabdi
11	489.5	19.2	542	1 CBP3 CANAL	P30574 candida alb
12	481.5	18.9	516	1 CPB3 HORVU	P52711 hordeum vul
13	479.5	18.8	469	1 YUW5 CAEL	P52717 caenorhabdi
14	471	18.4	508	1 YBY9 YEAST	P38109 saccharomyc
15	455	17.8	1002	1 CBP1 SCHPO	O13849 schizosacch
16	447.5	17.5	499	1 CBP1 HORVU	P07519 hordeum vul
17	446	17.5	482	1 NF31 NAEFO	P42651 naegleria f
18	442.5	17.3	523	1 CBP1 PICPA	P52210 pichia past
19	432.5	16.9	510	1 CBP1 ORISA	P37890 oryza sativ
20	432	16.9	532	1 CBP2 WHEAT	P00729 saccharomyc
21	428.5	16.8	423	1 CBP2 YEAST	P08819 triticum ae
22	426.5	16.7	436	1 CP22 HORVU	P55748 hordeum vul
23	425	16.6	452	1 RISC MOUSE	Q920a5 mus musculus
24	421.5	16.5	452	1 RISC RAT	Q920a6 rattus norv
25	413.5	16.2	476	1 CBP2 HORVU	P08818 hordeum vul
26	410	16.1	574	1 YPP3 CAEL	P52716 caenorhabdi
27	396	15.5	452	1 RISC HUMAN	Q9h340 homo sapien
28	395	15.5	470	1 YSS2 CAEL	Q09391 caenorhabdi
29	379.5	14.9	423	1 CPS1 PENJA	P14946 penicillium
30	376	14.7	729	1 KEX1 YEAST	P09620 saccharomyc
31	346	13.5	505	1 YXD2 CAEL	P52714 caenorhabdi
32	330.5	12.9	523	1 PEP3 ASPSA	P52719 aspergillus
33	309.5	12.1	507	1 SXA2 SCHPO	P32825 schizosacch

RESULT 1

ID	CPVL HUMAN	STANDARD;	PRT;	476 AA.
AC	Q9H3G5; Q9H3G5; Q9GAR7; Q9HB41;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Probable serine carboxypeptidase CPVL precursor (EC 3.4.16.-)			
DE	(Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase-like protein) (VCP-like protein).			
GN	CPVL OR VLP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=21295045; PubMed=11401439;			
RA	Maoney J.A., Ncolosi B., DaSilva R.P., Gordon S., McKnight A.J.;			
RT	"Cloning and characterization of CPVL, a novel serine carboxypeptidase, from human macrophages.";			
RL	Genomics 72:243-251(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Cho J.-J., Baik H.-H.;			
RT	"Cloning of VCP-like protein expressed in human heart and placenta.";			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,			
RA	Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,			
RA	Nagahari K., Sugano S., Isogai T.;			
RT	"HRI human cDNA sequencing project.";			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	MEDLINE=23388257; PubMed=12477932;			
RT	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

34	290	11.4	366	1	HNLS_SORBI
35	288.5	11.3	531	1	PEPF ASPNG
36	256	10.0	324	1	CP21_HORVU
37	245	9.6	286	1	CBPX_PEA
38	116.5	4.6	456	1	TRPE_LACLA
39	113	4.4	1516	1	MIS4_SCHPO
40	110.5	4.3	1048	1	SILA_SALTY
41	104.5	4.1	576	1	T2BR_BACSU
42	103.5	4.1	1562	1	YM81_YEAST
43	100.5	3.9	547	1	SYM_THEAC
44	99.5	3.9	1217	1	YHCE_BACSU
45	99	3.9	259	1	CAH2_TRIHK

P52708	sorghum bic
P52718	aspergillus
P55747	hordeum vul
Q41005	pisum sativ
Q02001	lactococcus
Q94477	schizosacch
Q9zhc9	salmonella
P06529	bacillus su
Q04781	saccharomyc
Q9hj12	thermoplasma
P54602	bacillus su
Q8uwa5	tribolodon

RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in the digestion of phagocytosed
 CC particles in the lysosome, participation in an inflammatory
 CC protease cascade, and trimming of peptides for antigen
 CC presentation.
 CC -!- TISSUE SPECIFICITY: Expressed in macrophages but not in other
 CC leukocytes. Abundantly expressed in heart and kidney. Also
 CC expressed in spleen, leukocytes, and placenta.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
 CC -----
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DR EMBL; AF106704; AAC37591.2; -;
 DR EMBL; AF282617; AAC14348.1; -;
 DR EMBL; AK075433; BAC11618.1; -;
 DR EMBL; BC016838; AAH16838.1; -;
 DR HSSP; P10619; 11VY.
 DR MEROPS; S10.003; -;
 DR Genew; HGNC:14399; CPVL.
 DR InterPro; IPR000379; Ser_estr_site.
 DR InterPro; IPR001563; Serine_catpept.
 DR Pfam; PF00450; serine_catpept; 1.
 DR PRINTS; PR00724; CRBOXYPASEC.
 DR ProDom; PD001189; Serine_catpept; 1.
 DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
 DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; FALSE_NEG.
 KW Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 ?
 FT CHAIN ? 476 PROBABLE SERINE CARBOXYPEPTIDASE CPVL.
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT ACT_SITE 388 388 BY SIMILARITY.
 FT ACT_SITE 448 448 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 25 25 R -> H (IN REF. 2).
 FT CONFLICT 284 284 L -> F (IN REF. 3 AND 4).
 FT CONFLICT 287 287 F -> L (IN REF. 3).
 FT CONFLICT 398 398 H -> R (IN REF. 3 AND 4).
 FT CONFLICT 422 422 F -> L (IN REF. 2).
 FT CONFLICT 435 435 A -> V (IN REF. 3 AND 4).
 FT CONFLICT 438 438 F -> S (IN REF. 2).
 SQ SEQUENCE 476 AA; 54110 MW; 2D966683A4F3FD01 CRC64;

Query Match 98.9%; Score 2527; DB 1; Length 476;
 Best Local Similarity 98.7%; Pred. No. 2.9e-177;
 Matches 470; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVGAMWKVTVSLVLLMPGCDGLFHSLYRSVSNPPKGDGQPLFTPTYEAGKIQKREL 60
 DB 1 MVGAMWKVTVSLVLLMPGCDGLFHSLYRSVSNPPKGDGQPLFTPTYEAGKIQKREL 60

QY 61 SLVGGPPGLNMSYAGFLTNKYNLSNLFWFPEAQIQEDAPVVLWLOGGGSSMXGL 120
 DB 61 SLVGGPPGLNMSYAGFLTNKYNLSNLFWFPEAQIQEDAPVVLWLOGGGSSMXGL 120

QY 121 FVEHGPPVYVTSNMTLRDRFPMTTXXSMLYIDNPVGTGFSFTDDTHGYAVNDDVARDLY 180
 DB 121 FVEHGPPVYVTSNMTLRDRFPMTTTLXSMLYIDNPVGTGFSFTDDTHGYAVNDDVARDLY 180

QY 181 SALIOFFQIFPEYKXNDFVVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAGDGY 240
 DB 181 SALIOFFQIFPEYKXNDFVVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAGDGY 240

RESULT 2

VCP_AEDAE STANDARD; PRT; 471 AA.
 ID VCP_AEDAE
 AC P42660;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vitellogenic carboxypeptidase precursor (EC 3.4.16.-).
 GN VCP.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-36.
 RC TISSUE=Fat body;
 RX MEDLINE=92073379; PubMed=1961751;
 RA Cho W.-L., Deitsch K.W., Raikhel A.S.;
 RT "An extraovarian protein accumulated in mosquito oocytes is a
 RT carboxypeptidase activated in embryos".
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10821-10824(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97242559; PubMed=9087558;
 RA Deitsch K.W., Raikhel A.S.;
 RT "Cloning and analysis of the locus for mosquito vitellogenic
 RT carboxypeptidase".
 RL Insect Mol. Biol. 2:205-213(1993).
 CC -!- FUNCTION: MAY PLAY A ROLE IN ACTIVATING HYDROLYTIC ENZYMES THAT
 CC ARE INVOLVED IN THE DEGRADATION OF YOLK PROTEINS IN DEVELOPING
 CC EMBRYOS OR MAY FUNCTION AS AN EXOPEPTIDASE IN THE DEGRADATION OF
 CC VITELLOGENIN.
 CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY OF VITELLOGENIC
 CC FEMALES, SECRETED INTO THE HEMOLYPH AND ACCUMULATES IN YOLK
 CC BODIES OF DEVELOPING OOCYTES.
 CC -!- DEVELOPMENTAL STAGE: MAXIMALLY PRESENT AT THE MIDDLE OF EMBRYONIC
 CC INDUCTION. BY 20-hydroxyecdysone.
 CC -!- PTM: ACTIVATION OF VCP IN EGGS IS ASSOCIATED WITH THE REDUCTION
 CC IN ITS SIZE FROM 53 kDa (INACTIVE FORM) TO 48 kDa (ACTIVE ENZYME).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
 CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINAL
 CC DUE TO A PUTATIVE FRAMESHIFT THAT MASKS THE LAST ACTIVE SITE
 CC RESIDUE.
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DR EMBL; M79452; AAA17682.1; -;
 DR EMBL; L46594; AAC41580.1; -;

DR PIR; A41612; A41612.
DR HSP; P10619; 11V.
DR MEROPS; S10.003; -.
DR InterPro; IPR000379; Ser. estrs. site.
DR InterPro; IPR001563; Serine_carbpept.
DR Pfam; PF00450; serine_carbpept; 1.
DR PRINTS; PR00724; CRBOXYPTASEC.
DR ProDom; PD001189; Serine carbpept; 1.
DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
KW Hydrolase; Carboxypeptidase; Glycoprotein; Hemolymph; Signal.
FT SIGNAL 1 19
FT CHAIN 20 471 VITELLOGENIC CARBOXYPEPTIDASE.
FT ACT SITE 207 207 BY SIMILARITY.
FT ACT SITE 391 391 BY SIMILARITY.
FT ACT SITE 448 448 BY SIMILARITY.
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CONFLICT 37 37 P -> R (IN REF. 1).
FT CONFLICT 136 136 K -> N (IN REF. 1).
FT CONFLICT 284 285 NS -> KC (IN REF. 1).
FT CONFLICT 426 471 GSIAGYKGRAGLQELIIRNAGHVMVPRDQKAFDMITSFT
HKNYL -> RKSPGTRSLGVCKRC (IN REF. 1).
SQ SEQUENCE 471 AA; 53676 MW; FDID0FBC15B2A7CE CRC64;
Query Match 39.7%; Score 1014; DB 1; Length 471;
Best Local Similarity 43.9%; Pred. No. 9.9e-67;
Matches 197; Conservative 95; Mismatches 145; Indels 12; Gaps 7;
QY 24 FHSLYRSVSMPPK-GDSGQPLFTPIEAGKIQKRELSLVGPFCLANKMSVAGFLTVNK 82
DB 26 YKLMRGSAAPRPGSGSEFLTLPLQDKIEAKRKARVNHVPMSSVESYSGFTVDA 85
QY 83 TYNLSMFLFFFAQIQEPDAPVVLWLGQGGSSMXGLFEVHGYPYVVTNMTLRDRDFW 142
DB 86 KENSNLFFWYVAKNREQAPILVWLGQGGGASSLFGMEENGPHIHRKSVKQREYSW 145
QY 143 TTTXSMLYIDNPVGTGFTDTHGYAVNEDVDVARDLYSALIQFOIPEYKNNDFYVTG 202
DB 146 HQNHMIYIDNPVGTGFTDTHGYAVNEDVDVARDLYSALIQFOIPEYKNNDFYVTG 205
QY 203 ESYAGKYVPAIAHLISLNPVREKINANGIAGDYSPESTIGYAEFLYQIGLDDK 262
DB 206 ESYGKGFVPAFYAIH-NSQOPKINLQGLAIGDGYDPLNQL-NYGEYELVELGLIDLN 262
QY 263 QKRYFOKQCEGIEHRIKQWFAFEILDKLDGLDTSPPSQVNTYFNFLRCTE 322
DB 263 GRKFDDEDTAALACAEKDMANFLIOGLFDG-LDQESYFKYTGTSYNYFIKGD 321
QY 323 PEDQ-LYYVKFSLPEVRAIHVGNQTFNDG---TIVEKYLREDTVQSVKPMLEIMNY 378
DB 322 ESKQSVLMFLSNPEVRKGIHVGLPFDHSDGNKVAEMLSEDTLDTVAPVWSKLLSHY 381
QY 379 KVLINYGOLDIIVAALATERSLGMGMDKWSQEKKAQKVKWIKFSDSEVAGVIRQVGF 438
DB 382 RVLYFNGOLDIICAYPMTVDFLMMKPFDDGSEYKRRANRIYRV---DGEIAGYKKGAGRL 438
QY 439 HOVIIRGGHILPYDOPALAFDMINRFY 467
DB 439 QEVLIIRNAGHVMVPRDQKAFDMITSFT 467
RESULT 3
CBP3 ORYSA
ID_CBP3 ORYSA STANDARD; PRT; 500 AA.
AC P37891;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine carboxypeptidase III precursor (EC 3.4.16.5).
GN CBP3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.
RX NCBI_TaxID=4530;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Yukihikari; TISSUE=Seed;
RX MEDLINE=92329723; PubMed=1627776;
RT Washio K., Ishikawa K.;
RA "Structure and expression during the germination of rice seeds of the
RT gene for a carboxypeptidase";
RL Plant Mol. Biol. 19:631-640(1992).
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
CC broad specificity.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- INDUCTION: BY GIBBERELIC ACID (GA). INHIBITED BY ABSICISIC ACID
CC (ABA).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
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DR EMBL; D10985; BAA01757.1; -.
DR PIR; S22530; S22530.
DR HSSP; P00729; 1YSC.
DR MEROPS; S10.009; -.
DR Gramene; P37891; -.
DR InterPro; IPR000379; Ser. estrs. site.
DR InterPro; IPR001563; Serine_carbpept.
DR Pfam; PF00450; serine_carbpept; 1.
DR PRINTS; PR00724; CRBOXYPTASEC.
DR ProDom; PD001189; Serine carbpept; 1.
DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
KW Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 21
FT CHAIN 22 73 BY SIMILARITY.
FT PROPEP 74 484 SERINE CARBOXYPEPTIDASE III.
FT PROPEP 485 500 BY SIMILARITY.
FT ACT SITE 216 216 BY SIMILARITY.
FT ACT SITE 404 404 BY SIMILARITY.
FT ACT SITE 461 461 BY SIMILARITY.
FT BINDING 407 407 SUBSTRATE (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 500 AA; 55446 MW; AE45SE2780147DB8 CRC64;
Query Match 22.9%; Score 585.5; DB 1; Length 500;
Best Local Similarity 29.6%; Pred. No. 2.2e-35;
Matches 149; Conservative 103; Mismatches 195; Indels 57; Gaps 15;
QY 1 MVGAMWKIVISLVLMFGPC-DGL-----FHSLYRSVSMPPK-----GDSG 40
DB 1 MATARVSILILVWLAASACAEGLRPRDAPFAAQAERLIRSNLLPKAGPTGAGD-- 58
QY 41 QPLFLTPYIEAGKIQKRELSLVGPFCL-NMKSVAGFLTVNKTYSNLSLFWFFFAQIQP 99
DB 59 -----VPSVAVGELLE-RRVTLPGLQGVGLGHGYYRLPNTHDARMFYLFESRGK 112
QY 100 EDAPVVLWLGQGGSSMXGLFEVHGYPYVVTNMTLRDRDPFTWTTXSMLYIDNPVGTGF 159
DB 113 ED-PVVIWLTGGPGCSSLAVFYENGPPPTISNNMSLAWNKFCWDITISNIFVDQDTGTF 171
QY 160 SFTDTHGYAVNEDVDVARDLYSALIQFOIPEYKNNDFYVTGESYAGKYVPAIAHLIS 219
DB 172 SYSSDDRDTRDETGVSNDLYSFLQVFFKGPHEFAKNDFFITGESYAGHYIPAFASRVHQ 231
QY 220 LNPVRE-VKINLINGIAGDYSDPESIIIGGYAEFLYQIGLDDKQKQYFQKQCEICBIH 278
DB 232 GNKANEIGHINLKGFAIGNGLTDPALQYKATVDALDMLNLLKSDYDRINKFIPPCFAI 291

QY 279 R-----KQWPEAFELDKLDGLTSDPSYFQNVGTGCSYNYFLRCTPEPDQLYV--- 329
 Db KLCGNGKASCAAYVNCNIF-----SIMKLVGTNYVDYVRK--ECEGKLCYDPS 341
 QY 330 --VKFSLPEVROAIHVGNQTF-NDGTIVEKYLRDVTQSVKPLWTEIM-NNYKVLIN 385
 Db 342 NLEKFFGDKAVRQAIQVGDIEFVSCSTTVYQAMLTDMNLEVGIPALLEDGINVLIVAG 401
 QY 386 QLDIIVAAALTEBSLGMGMKQSOEYKKAQKWKIFKSDSEVAGVIRQVGFPHOVIIRG 445
 Db 402 EYDLICNLWGNRWHSMWSQKDFVSSHESP---FVVDGAEAGVLSHGSLFLKVN 458
 QY 446 GGHILPYDQPLRAFDMINRFYIGK 469
 Db 459 AGHVMVPMQPKALEMLRFTQCK 482

RESULT 4

CBP3 HORVU STANDARD; PRT; 508 AA.
 AC P21529;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-MIII).
 GN CBP3 OR CXP.3.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Himalaya; TISSUE=Aleurone;
 RA Rocher A., Lok F., Cameron-Wills V., von Wettstein D.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 81-491.
 RC STRAIN=cv. Gula;
 RX MEDLINE=90315015; PubMed=2639682;
 RA Soerensen S.B., Svendsen I., Breddam K.;
 RT "Primary structure of carboxypeptidase III from malted barley."
 RL Carlsberg Res. Commun. 54:193-202(1989).
 CC -! CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
 broad specificity.
 CC -! ENZYME REGULATION: INHIBITED BY MERCURIC IONS.
 CC -! SUBUNIT: Monomer.
 CC -! SUBCELLULAR LOCATION: SECRETED INTO THE ENDOSPERM.
 CC -! DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN THE ALEURONE AND, TO A
 LESSER EXTENT IN THE EMBRYO, THROUGHOUT THE 5-DAYS GERMINATION
 PERIOD EXCLUSIVELY, WITH A MAXIMAL LEVEL AT 3 DAYS. ALSO FOUND IN
 THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
 CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.

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CC EMBL; Y09604; CAA70817.1; .
 DR HSP; P00729; 1CPV. .

DR MEROPS; S10.009; .

DR InterPro; IPR000379; Ser_estr_site.
 DR InterPro; IPR001563; Serine_carbpept.

DR Pfam; PF00450; serine_carbpept; 1.

DR PRINTS; PR00724; CRBOXPTASEC.

DR ProDom; PD001189; Serine_carbpept; 1.

DR PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.

DR PROSITE; PS00360; CARBOXYPEPT_SER_HIS; 1.

KW Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.

FT SIGNAL 1 19
 FT PROPEP 20 80
 FT CHAIN 81 491
 FT PROPEP 492 508
 FT MOD RES 81 81
 FT ACT SITE 223 223
 FT ACT SITE 411 411
 FT ACT SITE 468 468
 FT BINDING 414 414
 FT CARBOHYD 151 151
 FT VARIANT 265 265
 SQ SEQUENCE 508 AA; 56362 MW; 70C6751D78D40A56 CRC64;

Query Match 22.6%; Score 576; DB 1; Length 508;

Best Local Similarity 29.7%; Pred. No. 1.1e-34;
 Matches 150; Conservative 96; Mismatches 193; Indels 66; Gaps 15;

QY 9 IVSLVLLMP-----QPCDGLF-----HSLYRSVSMPPK---GDSGQPLFTPYIE 50
 Db LVSLLLALCAAAGALRLPPDASFPQAERLIRALLLPKSSSSGR-----H 58
 QY 51 AKTKQGRELSLVG-----PPGL-----NMKSYAGFLTVNKTYSNLFWFPPAQIQ 98
 Db 59 GARYGEGNEDEVAPGOLLERRVTLFGLPEGVADLGHAGYRLPNTHDARMEYFFESRGK 118
 QY 99 PEDAPVVLWLGQGGSGSMKGLFVEHGPVYVVTNMLRDRDFPMTTXXSMLYIDNPVGTG 158
 Db 119 KED-PVIVLTGGPCSSSELAFFVENGFFIANNMSLVNWKFGWDKISNIIFVDPQTGTG 177
 QY 159 FSFTDDTHGAVNEDDVARDLYSALIQFOIFPEYKNDNFYVTGESYAGKYVPAIAHLIH 218
 Db 178 PSYSSDDRDTRHDETVGSNDLYDFLQVFFKHPFIKNDFFITGESYAGHYIPAFASRVH 237
 QY 219 SLNPVRE-VKINLNGIAGDGYSDPESLIGGYAFLYQIGLLDEKQKFKQKQECIEH 277
 Db 238 QGNKKNEGTHINLKGFAIGNGLTDPATQYKAYTDYALEMNLIQADYERINKFIPTCEFA 297
 QY 278 IR-----KQWPEAFELDKLDGLTSDPSYFQNVGTGCSYNYFLRCTPEPDQLYV--- 329
 Db 298 IKLGTNGKASCAAYVNCNIFNS-----IMKLVGTNYVDYVRK--ECEGKLCYDF 347
 QY 330 ---VKFSLPEVROAIHVGNQTF-NDGTIVEKYLRDVTQSVKPLWTEIM-NNYKVLIN 384
 Db 348 SNLEKFFGDKAVRQAIQVGDIEFVSCSTSVYQAMLTDMNLEVGIPALLEDGINVLIV 407
 QY 385 QLDIIVAAALTEBSLGMGMKQSOEYKKAQKWKIFKSDSEVAGVIRQVGFPHOVIIR 444
 Db 408 GEYDLICNLWGNRWHSMWSQKDFAKTAE---SSFLVDDAAGVLSHGSLFLKVN 464
 QY 445 GGHILPYDQPLRAFDMINRFYIGK 469
 Db 465 NAGHVMVPMQPKALEMLRFTQCK 489

RESULT 5

CBPX ARATH

ID CBPX ARATH STANDARD; PRT; 516 AA.

AC P32826; Q42107; Q9CAE5.

DT 01-OCT-1993 (Rel. 27, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine carboxypeptidase precursor (EC 3.4.16.-).

GN AT3G10410 OR F13M14.32.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bradley D.;

RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.

RN [2]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 16:41:03 ; Search time 42 Seconds

(without alignments)
2924.596 Million cell updates/sec

Title: US-10-084-018-3

Perfect score: 2554

Sequence: 1 MYGAMWKVIVSLVLLMPGPC.....RAFDMINRFYKGMDDPYVG 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	70.6	434	11	Q9D3S9 mus musculus
2	1580	61.9	295	4	Q75225 homo sapien
3	1214	47.5	233	4	Q9NZ90 homo sapien
4	960.5	37.6	482	5	Q9VPT5 drosophila
5	839.5	32.9	434	5	Q81161 drosophila
6	623.5	24.4	444	10	Q9M9Q6 arabidopsis
7	582.5	22.8	508	10	Q8L6A7 theobroma c
8	581	22.7	505	10	Q9FB0 arabidopsis
9	577.5	22.6	507	10	Q8VWQ0 goessypium h
10	571.5	22.4	510	10	Q9LXH4 arabidopsis
11	567.5	22.2	501	10	Q9XH61 matricaria
12	564.5	22.1	510	10	Q932C3 arabidopsis
13	561	22.0	429	10	Q9LHX5 oryza sativ
14	556	21.8	429	10	Q8GV11 oryza sativ
15	556	21.8	548	4	Q9BR08 homo sapien
16	533.5	20.9	474	11	Q9D2D1 mus musculus

17	503	19.7	2105	5	Q17679
18	500	19.6	497	10	Q8L7B2
19	491	19.2	499	10	Q9FMK9
20	484	19.0	482	10	Q9SV04
21	473.5	18.5	494	10	Q9FEU4
22	473	18.5	504	10	Q9LSV8
23	470.5	18.4	452	10	Q9FP87
24	466.5	18.3	456	10	Q9SV78
25	466.5	18.3	501	10	Q9SV02
26	465.5	18.2	552	3	Q96VC4
27	463.5	18.1	2338	5	Q94269
28	462.5	18.1	479	10	Q949Q7
29	460.5	18.0	437	10	Q9FWG1
30	460.5	18.0	482	10	Q9FRJ0
31	460	18.0	502	10	Q9LY68
32	455.5	17.8	459	10	Q8RZS0
33	454.5	17.8	472	10	Q9LSM9
34	454.5	17.8	524	10	Q8GTK2
35	454	17.8	479	10	Q9MAR8
36	451	17.7	465	10	Q04084
37	439	17.2	498	10	Q9M513
38	435	17.0	490	10	Q9FYP7
39	434.5	17.0	456	10	Q9C7B2
40	432	16.9	425	10	Q82229
41	432	16.9	461	10	Q93Y09
42	431.5	16.9	458	10	Q22803
43	431	16.9	469	10	Q9FH06
44	430	16.8	459	10	Q9SPB5
45	429	16.8	452	10	Q9ZQ00

ALIGNMENTS

RESULT 1

Q9D3S9	PRELIMINARY;	PRT;	434 AA.
ID	Q9D3S9		
AC	Q9D3S9;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	4933436L16Rik protein.		
GN	4933436L16Rik.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Sakurai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK017087; BAB30589.1; --		
DR	HSSP; P08819; 1WHT.		

DR	MEROPS; S10.003; --
DR	InterPro; IPR001064; Crystallin.
DR	InterPro; IPR001563; Serine carboxpt.
DR	Pfam; PF00450; serine carboxpt; 1.
DR	PRINTS; PR00724; CRBOXPTASEC.
DR	ProDom; PD001189; Serine carboxpt; 1.
DR	PROSITE; PS00131; CARBOXYPEPT SER SER; 1.
DR	PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
FT	NON TER 1
SQ	SEQUENCE 295 AA; 34144 MW; FF7BEB265FA94983 CRC64;
Query Match	61.9%; Score 1580; DB 4; Length 295;
Best Local Similarity	99.7%; Pred.No. 5.7e-116;
Matches 294; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	182 ALIQFFOIFPEYKNDPFVVTGESVAGKYVPVAIAHLIHSLSNPVRVKLNGLAIAGDGYSD 241
Db	1 ALIQFFOIFPEYKNDPFVVTGESVAGKYVPVAIAHLIHSLSNPVRVKLNGLAIAGDGYSD 60
Qy	242 PESTIGGVAEFLYOIGLLDEBKQKKYFQKQCHECHIEHQRKNWFPAFEILDKLGDGLTSD 301
Db	61 PESTIGGVAEFLYOIGLLDEBKQKKYFQKQCHECHIEHQRKNWFPAFEILDKLGDGLTSD 120
Qy	302 PSYFQNVGTCSNYNFURCTEPEDQLYYVXFLSPLEVRQAITHVGNTPDNGDTIVEKYLRE 361
Db	121 PSYFQNVGTCSNYNLFURCTEPEDQLYYVXFLSPLEVRQAITHVGNTPDNGDTIVEKYLRE 180
Qy	362 DTQSVKVPWLTEIMNNYKVLIYNGOLDIIIVAAALTERSLMGMDWKGSOEYKKAEEKVWKI 421
Db	181 DTQSVKVPWLTEIMNNYKVLIYNGOLDIIIVAAALTERSLMGMDWKGSOEYKKAEEKVWKI 240
Qy	422 FKSDSEVAGVIROVDPHQVIIRGGGHILPYDQPLRAFDMINRRFYKGWDPPYVG 476
Db	241 FKSDSEVAGVIROVDPHQVIIRGGGHILPYDQPLRAFDMINRRFYKGWDPPYVG 295
RESULT 3	
ID Q9NZ90	PRELIMINARY; PRT; 233 AA.
AC Q9NZ90;	
DT 01-OCT-2000	(TrEMBLrel. 15, Created)
DT 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002	(TrEMBLrel. 20, Last annotation update)
DE	Uncharacterized bone marrow protein BM031.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RC	SEQUENCE FROM N.A.
TC	TISSUE=Bone marrow;
RX	MEDLINE=20493367; PubMed=11042152;
RA	Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA	Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA	Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT	"Cloning and functional analysis of cDNAs with open reading frames for
RT	300 previously undefined genes expressed in CD34+ hematopoietic
RT	stem/progenitor cells";
RL	Genome Res. 10:1546-1560(2000).
DR	EMBL; AF217508; AAF67619.1; -.
DR	HSSP; P10619; IIIV.
DR	MEROPS; S10.003; --
DR	InterPro; IPR001563; Serine carboxpt.
DR	Pfam; PF00450; serine carboxpt; 1.
DR	PRINTS; PR00724; CRBOXPTASEC.
DR	ProDom; PD001189; Serine carboxpt; 1.
DR	PROSITE; PS00131; CARBOXYPEPT SER SER; 1.
SQ	SEQUENCE 233 AA; 26901 MW; 17321A495485BA8 CRC64;
Query Match	47.5%; Score 1214; DB 4; Length 233;
Best Local Similarity	97.0%; Pred.No. 2.3e-87;
Matches 226; Conservative	0; Mismatches 7; Indels 0; Gaps 0;


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QY 117 MXGLFVEHGYVYVTSNMTLRDRFPWTTXSMYIDNPVGTGFSFTDDTHGYAVNEDVA 176
Db 1 MEGLFVEHGYVYVTSNMTLRDRFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDVA 60
QY 177 RLYSALIOFFQIFPPYKNDNFVVTGESYAGKVVPAINHLIHSNPNRVKINLNGIAG 236
Db 61 RLYSALIOFFQIFPPYKNDNFVVTGESYAGKVVPAINHLIHSNPNRVKINLNGIAG 120
QY 237 DGYSDPESIIIGGYAEFLYQIGLLDEKQKYFKQCHCEHTRKQNWFAFELDKLLDG 296
Db 121 DGYSDPESIIIGGYAEFLYQIGLLDEKQKYFKQCHCEHTRKQNWFAFELDKLLDG 180
QY 297 DUTSDPSYQNVTCGSNNYFNLCRTEPEDQLYVYKFLSLPEVRQAIHVGNQTF 349
Db 181 DUTSDPSYQNVTCGSNNYFNLCRTEPEDQLYVYKFLSLPEVRQAIHVGNQTF 233

RESULT 4
Q9VDT5
ID Q9VDT5 PRELIMINARY; PRT; 482 AA.
AC Q9VDT5;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG4572 protein (L047549P).
GN CG4572.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agayani A., An H.-O., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleab J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003728; AAF55705.1; --
DR EMBL; AY052032; AAK33446.1; --
DR HSSP; F10619; IIVI.
DR MEROPS; S10.003; --
DR FlyBase; FBgn0038738; CG4572.
DR InterPro; IPR001563; Serine carboxypeptidase.
DR InterPro; IPR000379; Ser esterase site.
DR Pfam; PF00450; serine carboxypeptidase; 1.
DR PRINTS; PR00724; CRBOXPTASEC.
DR PRODOM; PD001189; Serine carboxypeptidase; 1.
DR PROSITE; PS00560; CARBOXYPEPTIDASE; 1.
DR PROSITE; PS00131; CARBOXYPEPTIDASE; 1.
SQ SEQUENCE 482 AA; 54385 MW; 59E4B1A0E7B1C2B3 CRC64;

Query Match 37.6%; Score 960.5; DB 5; Length 482;
Best Local Similarity 44.4%; Pred. No. 5.3e-67;
Matches 196; Conservative 91; Mismatches 137; Indels 17; Gaps 8;

QY 38 DSGQPLFLTPYIEAGKIQKGRSLV---GPFGLNMKSYAGELTVNKTYSNLFPEWFF 93
Db 49 DPGEPLFLTPYIEAGKIQKGRSLV---GPFGLNMKSYAGELTVNKTYSNLFPEWFF 106
QY 94 PAQIQPEDAPVVLMLQGGPGSSMKXGFLVEHGYVYVTSNMTLRDRFPWTTXSMYIDN 153
Db 107 PAQIQPEDAPVVLMLQGGPGSSMKXGFLVEHGYVYVTSNMTLRDRFPWTTXSMYIDN 166
QY 154 PVGTGFTDTHGYAVNEDDVARLYSALIQFOIFPEYKNDNFVVTGESYAGKVVPAIN 213
Db 167 PVGTGFTDTHGYAVNEDDVARLYSALIQFOIFPEYKNDNFVVTGESYAGKVVPAIN 226
QY 214 AHLIHSNPNRVKINLNGIAGDGYSDPESIIIGGYAEFLYQIGLLDEKQKYFKQ 271
Db 227 AHLIHSNPNRVKINLNGIAGDGYSDPESIIIGGYAEFLYQIGLLDEKQKYFKQ 285
QY 272 HECIEHTRKQNWFAFELDKLLDGDLTSDPSYQNVTCGSNNYFNLCRTEPEDQLYVYK 331
Db 286 AKGAECSIKSHDMECAFVDSLSINGDLNG-SLFSNLGYNWYNYLK-THDDDCANLGE 343
QY 332 FLSLPEVRQAIHVGNQTFND---GTIVKYLREDTVQSKVPLTMINNYKVLINQGLD 388
Db 344 FLQAGATRAIHVGNKTFHDLDKENKVELHLKQIMDSVAPWIAELLARHTVCYISGQ 403
QY 389 IIVAAALTSRSLMGMDKSGOYKAEKKVKKPKSDSEVAGYIRQVGFHOVIIRGGH 448
Db 404 IIVAAALTSRSLMGMDKSGOYKAEKKVKKPKSDSEVAGYIRQVGFHOVIIRGGH 460
QY 449 ILPVDQPLRAFDIMNRFYIGK 469
Db 461 MAPHDQPKWLYNMIDHLTHYK 481

RESULT 5
Q9VDT5
ID Q9VDT5 PRELIMINARY; PRT; 434 AA.
AC Q9VDT5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG4572-PA (Fragment).
GN CG4572.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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